

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 17:39:01 ; Search time 8 Seconds
(without alignments)
131.089 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTRKAKNGAAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 17545 seqs, 3030971 residues

Total number of hits satisfying chosen parameters: 17545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
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3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326	17.3	355	US-11-135-855-44	Sequence 44, Appl
2	225	11.9	255	US-11-135-855-45	Sequence 45, Appl
3	98.5	5.2	574	US-10-821-234-1624	Sequence 1624, Ap
4	88.5	4.7	1560	US-11-059-982-1	Sequence 1, Appli
5	82.5	4.4	1493	US-11-004-057-21	Sequence 21, Appl
6	79.5	4.2	543	US-10-689-742-78	Sequence 78, Appl
7	78.5	4.2	1493	US-11-004-057-4	Sequence 4, Appli
8	77	4.1	2897	US-10-499-715-2	Sequence 2, Appli
9	75.5	4.0	328	US-10-821-234-1671	Sequence 1671, Ap
10	74.5	3.9	428	US-11-074-176-364	Sequence 364, App
11	74	3.9	345	US-10-821-234-1104	Sequence 1104, Ap
12	73.5	3.9	525	US-10-131-826A-56	Sequence 56, Appl
13	73.5	3.9	708	US-10-821-234-917	Sequence 917, App
14	71.5	3.8	1048	US-10-392-234A-20	Sequence 20, Appl
15	71	3.8	379	US-10-131-826A-216	Sequence 216, Appl
16	71	3.8	758	US-10-467-962B-12	Sequence 12, Appl
17	70.5	3.7	445	US-10-793-626-2858	Sequence 2858, Ap
18	70	3.7	552	US-10-821-234-1022	Sequence 1022, Ap
19	69.5	3.7	1299	US-10-821-234-1145	Sequence 1145, Ap
20	69	3.7	745	US-10-858-730-224	Sequence 224, App
21	69	3.7	1302	US-11-004-057-6	Sequence 6, Appli
22	68.5	3.6	1048	US-10-392-234A-14	Sequence 14, Appl
23	68	3.6	331	US-10-821-234-1650	Sequence 1650, Ap
24	67.5	3.6	242	US-10-821-234-1078	Sequence 1078, Ap
25	67.5	3.6	836	US-10-821-234-1559	Sequence 1559, Ap

26	67	3.6	153	1	US-10-821-234-1355	Sequence 1355, Ap
27	67	3.6	1107	7	US-11-057-058-41	Sequence 41, Appl
28	67	3.6	1476	1	US-10-647-956A-4	Sequence 4, Appli
29	66.5	3.5	325	1	US-10-131-826A-516	Sequence 516, App
30	66.5	3.5	396	7	US-11-109-156-10	Sequence 10, Appl
31	66	3.5	365	1	US-10-821-234-1575	Sequence 1575, Ap
32	66	3.5	488	1	US-10-984-376-1	Sequence 1, Appli
33	66	3.5	488	1	US-10-984-376-4	Sequence 4, Appli
34	65.5	3.5	211	7	US-11-132-839-12	Sequence 12, Appl
35	65.5	3.5	1049	1	US-10-392-234A-12	Sequence 12, Appl
36	65	3.4	745	1	US-10-131-826A-68	Sequence 68, Appl
37	65	3.4	745	7	US-11-135-855-37	Sequence 37, Appl
38	65	3.4	1970	1	US-10-821-234-1641	Sequence 1641, Ap
39	64	3.4	457	1	US-10-982-545-8	Sequence 8, Appli
40	64	3.4	457	1	US-10-982-545-13	Sequence 13, Appl
41	64	3.4	651	1	US-10-994-820A-34	Sequence 34, Appl
42	64	3.4	1467	1	US-10-821-234-1096	Sequence 1096, Ap
43	63.5	3.4	1048	1	US-10-392-234A-18	Sequence 18, Appl
44	63	3.3	317	1	US-10-131-826A-524	Sequence 524, App
45	63	3.3	401	1	US-10-821-234-881	Sequence 881, App

ALIGNMENTS

RESULT 1
US-11-135-855-44
; Sequence 44, Application US/11135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.1.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-44

Query Match 17.3%; Score 326; DB 7; Length 355;
Best Local Similarity 23.1%; Pred. No. 6.1e-25;
Matches 87; Conservative 42; Mismatches 95; Indels 152; Gaps 11;

QY	102	IGRGDEVCCAFCKVEIMRWEGDDPAADHRMAPOCPFVRKQMYANAGGEATVGRDEC-	160
DB	1	MGPXDSAKCLHRGPQSHWAAGDPTQE--RCGPR-----SLG--SPVLGLDTCR	46
QY	161	-----GASAA-TQPRMGPVHARYSTEARIATFKDPRRM	196
DB	47	AMDHVDGQILGQLRPLTEEEBEGAGATLSRGPAFG-----MGSEELRLASFYDWPLTA	101
QY	197	RQPEBELAAGFFYTGGDKTKFCYCDGGLKMWESDDVPWEQHARWFDRCAVYQLVKGRD	256
DB	102	EVPPELLAAAGFFHTGHQDKVRCFCYCGGLQSMKRGGDDPWTETHAKWFPSCQFLRSKGRD	161
QY	257	YIQKV-----	261
DB	162	FVHSVQETHSQLGWSVATSPRGSGWQGPAPISPFPDGLWLLPGPVGRTGRSPCGP	221
QY	262	-----KSEATA-----ISASEE	273

Db 222 LRSSLKVPRSQVQARDPLGEGWGRGGLRDPDLPWPPIEGGGQGVGTFRRPVLLGGVSPAEA 281
QY 274 EQA--ATNDSTKNVAQEGEKHLDDSKICKICYSEERNVCFVPCGHVAVACAKALSTDKC 330
Db 282 QRAWVWLEPFGARDVEAQ-LRRLQEERTCKVCLDRAVSIVFVPCGHLV-CAECAFGQLQLC 339
QY 331 PMCRRTFTNAVRLYFS 346
Db 340 PICRAPVRSRVRTFLS 355

RESULT 2
US-11-135-855-45

; Sequence 45, Application US/1135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for windows version 3.0
; SEQ ID NO 45
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-45

Query Match 11.9%; Score 225; DB 7; Length 255;
Best Local Similarity 31.7%; Pred. No. 2.8e-15;
Matches 53; Conservative 18; Mismatches 52; Indels 44; Gaps 6;

QY 102 LGRGDEVCAFCCKVEIMRWEGDDPADHRWARQCPFVRKQMYANAGGEATAGRDEC- 160
Db 1 MGRPKDSAKCLHRGPRQPSHWAAGDGPTE--RCGPR-----SLG--SPVLGLDTCR 46
QY 161 -----GASAA-TQPRMPGPVHARYSTEARLATFKDWRPM 196
Db 47 AWDHVDGQILGQLRPLTEEEEGAGATLSRGPAFPG-----MGSEELRLASFYDWPLTA 101
QY 197 RQKPEELAEAGFFYTGGGDKTKCFYCDGGLKDWESDDVPEQHARWF 243
Db 102 EVPELLAAAGFFHTGHQDKVRCFCYGGGLQSWKRGDDPWTETHAKWF 148

RESULT 3

US-10-821-234-1624
; Sequence 1624, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes version 1.0

; SEQ ID NO 1624
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1624

Query Match 5.2%; Score 98.5; DB 1; Length 574;
Best Local Similarity 34.0%; Pred. No. 0.016;
Matches 18; Conservative 6; Mismatches 24; Indels 5; Gaps 1;

QY 299 KICCYSEERNVCFVPCGHVAVACAKALSTDK-----CPMCRRTFTNAVRLYFS 346
Db 521 CTICYEHAVDTVIYTCGHMCLCYACGLRLKALHACCPICRRPIKDIITYRS 573

RESULT 4
US-11-059-982-1

; Sequence 1, Application US/11059982
; Publication No. US20050255507A1
; GENERAL INFORMATION:
; APPLICANT: Jenkins, Robert B.
; APPLICANT: Yang, Ping
; APPLICANT: Thibodeau, Steve
; APPLICANT: Wang, Liang
; APPLICANT: Schaid, Daniel
; TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
; FILE REFERENCE: 07039-505001
; CURRENT APPLICATION NUMBER: US/11/059,982
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,573
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for windows version 4.0
; SEQ ID NO 1
; LENGTH: 1560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-059-982-1

Query Match 4.7%; Score 88.5; DB 7; Length 1560;
Best Local Similarity 29.4%; Pred. No. 0.56;
Matches 37; Conservative 12; Mismatches 48; Indels 29; Gaps 7;

QY 121 VEGDDPADHRR--WAPQCPF--VRKQMYANAGG----EATAVGRDEGASATQPPRM 171
Db 1363 VDHPPPAAPERKPLGTAPHCPRLPLRKYRENVGGPAGPEGTAGRARGS-----PAPL 1417
QY 172 PGPVHARYSTEARLATFKD--WPRRMROKPEELAEAGFFYTGGGDKTKCFYCDGGLKDW 229
Db 1418 PAKVDEATSGLIRELAAVEDELYQRMKGPBPPEPASA--AQGTGD-----PDW 1464
QY 230 ESDDVP 235
Db 1465 EAPGLP 1470

RESULT 5

US-11-004-057-21
; Sequence 21, Application US/11004057
; Publication No. US20050244846A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Gary L.
; TITLE OF INVENTION: MEK1 PROTEINS AND FRAGMENTS THEREOF FOR USE IN REGULATING
; FILE REFERENCE: CPI-042CPC
; CURRENT APPLICATION NUMBER: US/11/004,057
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/09/403,075
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21

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OM protein - protein search, using bw model

Run on: November 26, 2005, 17:38:31 ; Search time 77 Seconds
(without alignments)
1877.519 Million cell updates/sec

Title: US-10-041-859a-2

Perfect score: 1887

Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	346	4	US-10-041-859-2 Sequence 2, Appli
2	966	51.2	275	3	US-09-201-936-12 Sequence 12, Appl
3	966	51.2	275	4	US-10-323-643-9 Sequence 9, Appli
4	966	51.2	275	4	US-10-600-272-12 Sequence 12, Appl
5	932.5	49.4	172	4	US-10-041-859-8 Sequence 8, Appli
6	862	45.7	268	4	US-10-323-643-10 Sequence 10, Appl
7	846.5	44.9	172	4	US-10-041-859-10 Sequence 10, Appl
8	831.5	44.1	172	4	US-10-041-859-9 Sequence 9, Appli
9	767.5	40.7	263	5	US-10-706-635-15 Sequence 15, Appl
10	759.5	40.2	172	4	US-10-041-859-11 Sequence 11, Appl
11	719.5	38.1	438	4	US-10-267-502-419 Sequence 419, App
12	719.5	38.1	438	6	US-11-097-143-12366 Sequence 12366, A
13	719.5	38.1	438	6	US-11-097-143-28833 Sequence 28833, A
14	696.5	36.9	172	4	US-10-041-859-12 Sequence 12, Appl
15	554.5	29.4	172	4	US-10-041-859-13 Sequence 13, Appl
16	526.5	27.9	604	4	US-10-232-286-4 Sequence 4, Appli
17	526.5	27.9	604	4	US-10-141-618-6 Sequence 6, Appli
18	526.5	27.9	604	4	US-10-366-307-6 Sequence 6, Appli
19	526.5	27.9	604	4	US-10-730-476A-79 Sequence 79, Appl
20	526.5	27.9	604	5	US-10-825-282-40 Sequence 40, Appl
21	526.5	27.9	604	5	US-10-934-717-4 Sequence 4, Appli
22	526.5	27.9	604	5	US-10-485-225-22 Sequence 22, Appl
23	526.5	27.9	604	5	US-10-730-476A-79 Sequence 79, Appl
24	525.5	27.8	600	3	US-09-974-592-12 Sequence 12, Appl
25	525.5	27.8	600	5	US-10-482-952-1 Sequence 1, Appli
26	524.5	27.8	604	3	US-09-974-592-6 Sequence 6, Appli
27	524.5	27.8	604	3	US-09-201-936-6 Sequence 6, Appli

28	524.5	27.8	604	4	US-10-636-065-221	Sequence 221, App
29	524.5	27.8	604	4	US-10-600-272-6	Sequence 6, Appli
30	517.5	27.4	602	3	US-09-201-936-40	Sequence 40, Appl
31	517.5	27.4	602	4	US-10-636-065-227	Sequence 227, App
32	517.5	27.4	602	4	US-10-600-272-40	Sequence 40, Appli
33	507.5	26.9	618	3	US-09-974-592-8	Sequence 8, Appli
34	507.5	26.9	618	3	US-09-201-936-8	Sequence 8, Appli
35	507.5	26.9	618	4	US-10-636-065-223	Sequence 223, App
36	507.5	26.9	618	4	US-10-600-272-8	Sequence 8, Appli
37	500.5	26.5	498	3	US-09-201-936-13	Sequence 13, Appl
38	500.5	26.5	498	4	US-10-600-272-13	Sequence 13, Appl
39	500.5	26.5	618	4	US-10-153-668-338	Sequence 338, App
40	500.5	26.5	618	4	US-10-207-655-200	Sequence 200, App
41	500.5	26.5	618	4	US-10-232-286-2	Sequence 2, Appli
42	500.5	26.5	618	4	US-10-366-307-4	Sequence 4, Appli
43	500.5	26.5	618	4	US-10-361-270-3	Sequence 3, Appli
44	500.5	26.5	618	4	US-10-260-708-63	Sequence 63, Appl
45	500.5	26.5	618	4	US-10-730-476A-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1
US-10-041-859-2
; Sequence 2, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041, 859
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260, 478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Bombyx mori
; US-10-041-859-2

Query Match	100.0%;	Score 1887;	DB 4;	Length 346;
Best Local Similarity	100.0%;	Pred. No. 1.7e-169;		
Matches 346;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MELTKVAKNGAATLVMLKNARDAKMRPFGLMLSSCESSSTSTLPSSSADKTNDND	60	
Db	1	MELTKVAKNGAATLVMLKNARDAKMRPFGLMLSSCESSSTSTLPSSSADKTNDND	60	
QY	61	TFNFLPDMPPMRREERLKTFDQWPVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRW	120	
Db	61	TFNFLPDMPPMRREERLKTFDQWPVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRW	120	
QY	121	VEGDDPADHRRWAPQCFVVRKOMYANAGGEATVGRDECASASATQPRMGPVHARYS	180	
Db	121	VEGDDPADHRRWAPQCFVVRKOMYANAGGEATVGRDECASASATQPRMGPVHARYS	180	
QY	181	TEARLATFKDWPRMRQKPEELAEAGFFYTGQDKTKCFYCDGLKDWESDDVPWEQHA	240	
Db	181	TEARLATFKDWPRMRQKPEELAEAGFFYTGQDKTKCFYCDGLKDWESDDVPWEQHA	240	
QY	241	RWFDRCAYVOLVKGRDYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDSKICK	300	
Db	241	RWFDRCAYVOLVKGRDYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDSKICK	300	
QY	301	ICYSEBRNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS	346	

Db 301 ICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 2

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US-09-201-936-12
; Sequence 12, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
US-09-201-936-12
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Query Match 51.2%; Score 966; DB 3; Length 275;
Best Local Similarity 59.2%; Pred. No. 1.4e-82;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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QY 68 MPDMRREERLKTFFDQWVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRWEGDDPA 127
Db 1 MSDLRLLEVRLLNTFEKMPVSVFLSPETMAKNGFYLLGRSDEVRCAFCKVEIMRWKEGEDPA 60

QY 128 ADHRWAPQCPEVRKQMYANAGGEATAVGRDECGASATQ-----PPRMGPVHARYS 180
Db 61 ADHKWAPQCPEVK-----GIDVCGSIVTTNNIQNTTHTDTITIGPAHPKYA 106

QY 181 TEARLATFKDWRPRMRQKPEELAEAGFFYTGGDKTKCFYCDGGLKDWESDVPWEQHA 240
Db 107 HEARVKSFHNNWPRCKORPEQADAGFFYTGYGDNTKCFYCDGGLKDWEPEDVPWEQHV 166

QY 241 RWFDRCAVYQLVKGRDYIQVKSEATAI--SASEEQATNDSTKNVAOEGEKHLDDSK 297
Db 167 RWFDRCAVYQLVKGRDYQKVITEACVLPGENTTVSTAAPVSEPIPETKIEKEPQVEDSK 226

QY 298 ICKICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
Db 227 LCKICYVEECIVCFVPCGHVAVACAKCALSVDKCPMCRKIIVTSVLKYFS 275
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RESULT 3

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US-10-323-643-9
; Sequence 9, Application US/10323643
; Publication No. US20030108552A1
; GENERAL INFORMATION:
; APPLICANT: He, et al.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; FILE REFERENCE: PF165PID1
; CURRENT APPLICATION NUMBER: US/10/323,643
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 08/464,588
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US95/05922
; PRIOR FILING DATE: 1995-05-11
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella granulovirus
US-10-323-643-9
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Query Match 51.2%; Score 966; DB 4; Length 275;
Best Local Similarity 59.2%; Pred. No. 1.4e-82;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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QY 68 MPDMRREERLKTFFDQWVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRWEGDDPA 127
Db 1 MSDLRLLEVRLLNTFEKMPVSVFLSPETMAKNGFYLLGRSDEVRCAFCKVEIMRWKEGEDPA 60

QY 128 ADHRWAPQCPEVRKQMYANAGGEATAVGRDECGASATQ-----PPRMGPVHARYS 180
Db 61 ADHKWAPQCPEVK-----GIDVCGSIVTTNNIQNTTHTDTITIGPAHPKYA 106

QY 181 TEARLATFKDWRPRMRQKPEELAEAGFFYTGGDKTKCFYCDGGLKDWESDVPWEQHA 240
Db 107 HEARVKSFHNNWPRCKORPEQADAGFFYTGYGDNTKCFYCDGGLKDWEPEDVPWEQHV 166

QY 241 RWFDRCAVYQLVKGRDYIQVKSEATAI--SASEEQATNDSTKNVAOEGEKHLDDSK 297
Db 167 RWFDRCAVYQLVKGRDYQKVITEACVLPGENTTVSTAAPVSEPIPETKIEKEPQVEDSK 226

QY 298 ICKICYSEERNVCFVPCGHVAVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
Db 227 LCKICYVEECIVCFVPCGHVAVACAKCALSVDKCPMCRKIIVTSVLKYFS 275
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RESULT 4

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US-10-600-272-12
; Sequence 12, Application US/10600272
; Publication No. US20040157232A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003006
; CURRENT APPLICATION NUMBER: US/10/600,272
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/011,356
; PRIOR FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: PCT/IB96/01022
; PRIOR FILING DATE: 1996-08-05
; PRIOR APPLICATION NUMBER: US 08/576,956
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: US 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
US-10-600-272-12
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Query Match 51.2%; Score 966; DB 4; Length 275;
Best Local Similarity 59.2%; Pred. No. 1.4e-82;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

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QY 68 MPDMRREERLKTFFDQWVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRWEGDDPA 127
Db 1 MSDLRLLEVRLLNTFEKMPVSVFLSPETMAKNGFYLLGRSDEVRCAFCKVEIMRWKEGEDPA 60

QY 128 ADHRWAPQCPEVRKQMYANAGGEATAVGRDECGASATQ-----PPRMGPVHARYS 180
Db 61 ADHKWAPQCPEVK-----GIDVCGSIVTTNNIQNTTHTDTITIGPAHPKYA 106
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 17:34:56 ; Search time 29 Seconds
(without alignments)
986.406 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDCPCMGCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1311	69.5	377	2	US-09-502-528-3 Sequence 3, Appli
2	966	51.2	275	1	US-08-511-485-12 Sequence 12, Appl
3	966	51.2	275	2	US-08-836-134-21 Sequence 21, Appl
4	966	51.2	275	2	US-09-493-784-21 Sequence 21, Appl
5	966	51.2	275	2	US-09-201-936-12 Sequence 12, Appl
6	966	51.2	275	2	US-09-011-356-12 Sequence 12, Appl
7	966	51.2	275	2	US-09-201-932-12 Sequence 12, Appl
8	862	45.7	268	2	US-08-836-134-22 Sequence 22, Appl
9	862	45.7	268	2	US-09-493-784-22 Sequence 22, Appl
10	767.5	40.7	263	2	US-09-662-254B-15 Sequence 15, Appl
11	725.5	38.4	438	2	US-09-586-305A-12 Sequence 12, Appl
12	723.5	38.3	438	2	US-09-586-305A-11 Sequence 11, Appl
13	723.5	38.3	438	2	US-09-586-305A-13 Sequence 13, Appl
14	717.5	38.0	438	2	US-09-586-305A-14 Sequence 14, Appl
15	717.5	38.0	438	2	US-09-586-305A-15 Sequence 15, Appl
16	715.5	37.9	438	2	US-09-586-305A-19 Sequence 19, Appl
17	713.5	37.8	438	2	US-09-586-305A-20 Sequence 20, Appl
18	712.5	37.8	438	2	US-09-586-305A-16 Sequence 16, Appl
19	712.5	37.8	438	2	US-09-586-305A-17 Sequence 17, Appl
20	531.5	28.2	431	2	US-09-586-305A-18 Sequence 18, Appl
21	526.5	27.9	604	2	US-08-569-749-4 Sequence 4, Appli
22	526.5	27.9	604	2	US-09-949-016-6031 Sequence 6031, Ap
23	526.5	27.9	604	2	US-09-689-366-4 Sequence 4, Appli
24	526.5	27.9	604	2	US-10-232-286-4 Sequence 4, Appli
25	526.5	27.9	604	4	PCT-US96-12860-4 Sequence 4, Appli
26	526.5	27.9	613	2	US-09-949-016-10878 Sequence 10878, A
27	525.5	27.8	600	2	US-09-212-971-12 Sequence 12, Appl

28	525.5	27.8	600	2	US-08-800-929A-12	Sequence 12, Appl
29	525.5	27.8	600	2	US-09-617-053A-12	Sequence 12, Appl
30	524.5	27.8	604	1	US-08-511-485-6	Sequence 6, Appli
31	524.5	27.8	604	2	US-09-212-971-6	Sequence 6, Appli
32	524.5	27.8	604	2	US-08-800-929A-6	Sequence 6, Appli
33	524.5	27.8	604	2	US-09-617-053A-6	Sequence 6, Appli
34	524.5	27.8	604	2	US-09-011-936-6	Sequence 6, Appli
35	524.5	27.8	604	2	US-09-011-356-6	Sequence 6, Appli
36	524.5	27.8	604	2	US-09-672-717-221	Sequence 221, App
37	524.5	27.8	604	2	US-09-201-932-6	Sequence 6, Appli
38	517.5	27.4	602	2	US-09-201-936-40	Sequence 40, Appl
39	517.5	27.4	602	2	US-09-011-356-40	Sequence 40, Appl
40	517.5	27.4	602	2	US-09-672-717-227	Sequence 227, App
41	517.5	27.4	602	2	US-09-201-932-40	Sequence 40, Appl
42	507.5	26.9	618	1	US-08-511-485-8	Sequence 8, Appli
43	507.5	26.9	618	2	US-09-212-971-8	Sequence 8, Appli
44	507.5	26.9	618	2	US-08-800-929A-8	Sequence 8, Appli
45	507.5	26.9	618	2	US-09-617-053A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-502-528-3
; Sequence 3, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfiAP)
US-09-502-528-3

Qy	Query Match	69.5%;	Score 1311;	DB 2;	Length 377;
Db	Best Local Similarity	68.5%;	Pred. No. 3.2e-128;		
	Matches 248;	Conservative 39;	Mismatches 57;	Indels 18;	Gaps 7;
Qy	1 MELTKVAKNGAATLVMLKN-ARDAKMRPFIQPLML--SSCESSTSTLSPSS-----	51			
Db	18 MDITKVASNGSSSTLTLPKSGSLEAKIRP-LAPLMLPTPSYDSNAGSPSLSPSTPCSSS	76			
Qy	52 -SADKTDNHTFNFLLPDMRMRREERLKTFDQWPVTFLLTPQOLARNGFYTLGRDEVCC	110			
Db	77 FSIDKTDNHTFNGFSADTVDMRKEDEMRKTFEKMPVSFLSGEQLARNGFYTLGRDEARC	136			
Qy	111 AFCKVEIMRWVEGDDPADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAA---TQ	167			
Db	137 AFCKVEIMRWVEGDDPADHQRWAPQCPFVRK-LNGTAAADTGSSGQDECGARAPSGTS	195			
Qy	168 PPRMPGPVHARYSTEARLATFKDWMRRMRQKPEELAEAGFFYTGQDKTKCFYCDGLK	227			
Db	196 PPRMAGPVHPRYASAEARLRSFKDWMRCMRQKPEELAEAGFFYTGQDKTKCFYCDGLK	255			
Qy	228 DWESDDVPWEQHARWFDRCAYVQLVKGSDYIQKVSSEATAISASEEQ---AATNDSTKN	284			
Db	256 DWENHDVPWEQHARWFDRCAYVQLVKGREYVQKVISAECEVSASEARDVAPARTAEPS	315			
Qy	285 VAQGEKHLDDSKICKICYSEERNVCFVPCGHVACAKCALSTDKCPMCRRTFTNAVRLY	344			

Db 316 PAEAPENSVDSDSKLCKICIAEERNVCFVPCGHVAVACAKCALADKCPMCRRTFQNAVRLY 375

Qy 345 FS 346

Db 376 FS 377

RESULT 2

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US-08-511-485-12
; Sequence 12, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-12

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Query Match	51.2%;	Score 966;	DB 1;	Length 275;
Best Local Similarity	59.2%;	Pred. No. 2.2e-92;		
Matches 171;	Conservative 39;	Mismatches 55;	Indels 24;	Gaps 3;

[illegible]

Db 227 LCKICYVEECIVCFVPCGHVACAKCALSDKCPMCRKIVTSVLKVFSS 275

RESULT 3

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US-08-836-134-21
; Sequence 21, Application US/08836134A
; Patent No. 6020127
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, Joh-e
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6020127
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/08/836,134A
; CURRENT FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Cydia pomonella
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-08-836-134-21

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Query Match	51.2%;	Score 966;	DB 2;	Length 275;
Best Local Similarity	59.2%;	Pred. No. 2.2e-92;		
Matches 171;	Conservative 39;	Mismatches 55;	Indels 24;	Gaps 3;

[illegible]

RESULT 4

US-09-493-784-21
; Sequence 21, Application US/09493784
; Patent No. 6429011
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: Mclean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, Joh-e
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6429011
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/09/493,784
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 08/836,134

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 26, 2005, 17:26:11 ; Search time 24 Seconds
(without alignments)
1387.125 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	966	51.2	275	2	A45679	inhibitor-of-apopt
2	862	45.7	268	2	T10304	inhibitor of apopt
3	862	45.7	268	2	A53989	apoptosis-inhibiti
4	542	28.7	358	2	JC5964	apoptosis inhibito
5	524.5	27.8	604	2	S68449	apoptosis inhibito
6	507.5	26.9	618	2	S68450	apoptosis inhibito
7	501	26.6	497	2	S69545	apoptosis inhibito
8	500.5	26.5	496	2	S68452	apoptosis inhibito
9	497.5	26.4	497	2	S69544	apoptosis inhibito
10	381.5	20.2	292	2	T41772	IAP1 orf27 - Bomby
11	378	20.0	286	2	D36828	orf13 protein - Au
12	369.5	19.6	275	2	T10310	apoptosis-inhibiti
13	362.5	19.2	298	2	JC7568	kidney inhibitor o
14	309	16.4	1447	2	T42628	neuronal apoptosis
15	299	15.8	1232	2	A55478	neuronal apoptosis
16	253	13.4	208	2	T03183	probable apoptosis
17	252.5	13.4	150	2	T28409	ORF MSV248 probabl
18	232	12.3	234	2	T30427	probable apoptosis
19	222.5	11.8	155	2	T30489	apoptosis inhibito
20	220.5	11.7	997	2	T43523	cut17 protein - fi
21	171.5	9.1	308	2	T37474	apoptosis inhibito
22	164.5	8.7	249	2	T41814	IAP2 orf71 - Bomby
23	164.5	8.7	329	2	T28403	ORF MSV242 probabl
24	159.5	8.5	249	2	H72858	apoptosis inhibito
25	156	8.3	236	2	T10343	inhibitor of apopt
26	155.5	8.2	383	2	F96582	hypothetical prote
27	154	8.2	4845	2	T31067	BIR repeat contain
28	149.5	7.9	115	2	B96664	probable RING zinc
29	139	7.4	124	2	T01251	hypothetical prote

30	132.5	7.0	864	2	T01393	apoptosis inhibito
31	131.5	7.0	489	2	S15349	mdm2 protein - mou
32	130	6.9	428	2	T48167	hypothetical prote
33	122.5	6.5	237	2	T52432	hypothetical prote
34	122.5	6.5	823	2	D86165	protein F15K9.3 li
35	120	6.4	711	2	C84767	hypothetical prote
36	120	6.4	943	2	S68824	rn8 protein, cyto
37	119	6.3	433	2	JC7678	RING finger protei
38	117	6.2	491	1	S24354	p53-binding protei
39	116	6.1	754	2	S35503	finger protein neu
40	115	6.1	401	2	G96824	hypothetical prote
41	115	6.1	529	2	T19204	hypothetical prote
42	114	6.0	337	2	T48341	hypothetical prote
43	114	6.0	372	2	C96631	hypothetical prote
44	113.5	6.0	269	2	T40371	probable zinc fing
45	112	5.9	204	2	T01447	hypothetical prote

ALIGNMENTS

RESULT 1
A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpgV
C;Species: Cydia pomonella granulosis virus CpgV
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A45679
R;Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A;Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif.
A;Reference number: A45679; MUID:93188168; PMID:8445726
A;Accession: A45679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <CRO>
A;Cross-references: UNIPROT:P41436; UNIPARC:UP1000012D0CE; GB:L05494; NID:9289583; PIDN:J
A;Note: Sequence extracted from NCBI backbone (NCBIN:127014, NCBI:P:127015)
C;Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match 51.2%; Score 966; DB 2; Length 275;
Best Local Similarity 59.2%; Pred. No. 2.2e-73;
Matches 171; Conservative 39; Mismatches 55; Indels 24; Gaps 3;

QY	68	MDMRREBERLKTFDQWPTFLTPBQLARNGFYILGRGDEVCCAFCKVEIMRWEGDDPA	127
DB	1	MSDLRLIEVRLNTFEKWPVSFLSPETMAKNGFYILGRSDEVRCAPCKVEIMRWEGEDPA	60
QY	128	ADHRRWAPQCPFVRKQWYANAGGEATAVGRDECGASAATQ-----PRMPGVHARYS	180
DB	61	ADHKWAPQCPFVK-----GIDVCGSIYTTNNIQTTHDTTIGPAHPKYA	106
QY	181	TEARLATFKDWRPRMRQPEELAEAGFFYTGQGDTKCFYCDGGLKDWESDVPWEQHA	240
DB	107	HEARVKSFHNWPRCMQRPBQADAGFFYTGDMTKCFYCDGGLKDWEPEDVPEQHV	166
QY	241	RMFDRCAVYQLVKGRDYIQVKSEATAI---SASEEQAAATNDSTKNVAQEGEKHLDDSK	297
DB	167	RMFDRCAVYQLVKGRDYQKVIITACVLPGENTIVSTAAPVSEPIPETKIEKEPEVEDSK	226
QY	298	ICKICYSEERNVCFVPCGHVACAKALSTDKCPMCRRTFTNAVRLYFS	346
DB	227	LCKICVVEECIVCFVPCGHVACAKALSVDKCPMCRKIVTSVLKVYFS	275

RESULT 2
T10304
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C;Accession: T10304
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis



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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 26, 2005, 16:55:00 ; Search time 6.5 Seconds
(without alignments)
3518.724 Million cell updates/sec

Title: US-10-041-859A-1
Perfect score: 6692
Sequence: 1 cattattaactcacttcac.....tcgcgctctactctctgtga 3773

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 17545 segs, 3030971 residues

Total number of hits satisfying chosen parameters: 35090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10041859 @CGN_1_1_1 @runat_23112005_100315_12004
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep: *
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: *
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	4.9	355	US-11-135-855-44	Sequence 44, Appl
2	230	3.4	255	US-11-135-855-45	Sequence 45, Appl
3	98.5	1.5	574	US-10-821-234-1624	Sequence 1624, Ap
4	95.5	1.4	540	US-10-821-234-1456	Sequence 1456, Ap
5	94.5	1.4	993	US-11-137-465-36	Sequence 36, Appl
6	90	1.3	2432	US-10-821-234-899	Sequence 899, Appl
7	89.5	1.3	428	US-11-074-176-364	Sequence 364, Appl
8	89.5	1.3	1560	US-11-059-982-1	Sequence 1, Appl1
9	88.5	1.3	1133	US-10-821-234-1219	Sequence 1219, Ap
10	87	1.3	1493	US-11-004-057-4	Sequence 4, Appl1

11	86	1.3	1493	7	US-11-004-057-21	Sequence 21, Appl
12	84.5	1.3	2432	1	US-10-821-234-899	Sequence 899, Appl
13	82.5	1.2	543	1	US-10-689-742-78	Sequence 78, Appl
14	82	1.2	468	1	US-10-793-626-868	Sequence 868, Appl
15	82	1.2	468	1	US-10-793-626-1618	Sequence 1618, Ap
16	82	1.2	1075	1	US-10-821-234-1202	Sequence 1202, Ap
17	79	1.2	339	7	US-11-010-874-3	Sequence 3, Appl1
18	79	1.2	1302	7	US-11-004-057-6	Sequence 6, Appl1
19	78.5	1.2	259	1	US-10-131-826A-300	Sequence 300, Appl
20	78.5	1.2	259	7	US-11-182-946-2	Sequence 2, Appl1
21	78.5	1.2	331	1	US-10-821-234-1650	Sequence 1650, Ap
22	78	1.2	258	7	US-11-054-515-1274	Sequence 1274, Ap
23	78	1.2	514	1	US-10-821-234-998	Sequence 998, Appl
24	78	1.2	579	1	US-10-821-234-1352	Sequence 1352, Ap
25	77.5	1.2	477	1	US-10-131-826A-50	Sequence 50, Appl
26	77.5	1.2	953	7	US-11-057-058-53	Sequence 53, Appl
27	77.5	1.2	953	7	US-11-057-058-57	Sequence 57, Appl
28	77	1.2	2897	1	US-10-499-715-2	Sequence 2, Appl1
29	76.5	1.1	138	1	US-10-667-295-176	Sequence 176, Appl
30	76.5	1.1	559	1	US-10-821-234-947	Sequence 947, Appl
31	76.5	1.1	708	1	US-10-821-234-917	Sequence 917, Appl
32	76.5	1.1	895	7	US-11-150-406-2	Sequence 2, Appl1
33	76.5	1.1	920	1	US-10-821-234-1129	Sequence 1129, Ap
34	76.5	1.2	1142	7	US-11-044-051-73	Sequence 73, Appl
35	76	1.1	173	1	US-10-667-295-9	Sequence 9, Appl1
36	76	1.1	419	1	US-10-821-234-1556	Sequence 1556, Ap
37	76	1.1	525	1	US-10-131-826A-56	Sequence 56, Appl
38	76	1.1	587	1	US-10-925-970-6	Sequence 6, Appl1
39	76	1.2	761	1	US-10-485-517-252	Sequence 252, Appl
40	75.5	1.1	328	1	US-10-821-234-1671	Sequence 1671, Appl
41	75.5	1.1	937	7	US-11-057-058-55	Sequence 55, Appl
42	75	1.1	575	1	US-10-131-826A-128	Sequence 128, Appl
43	75	1.1	690	1	US-10-131-826A-306	Sequence 306, Appl
44	74.5	1.1	339	7	US-11-010-874-2	Sequence 2, Appl1
45	74.5	1.1	648	1	US-10-793-626-1060	Sequence 1060, Ap

ALIGNMENTS

RESULT 1
US-11-135-855-44
; Sequence 44, Application US/1135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135, 855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203, 708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-44
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Score: 331.00
Percent Similarity: 36.79%
Best Local Similarity: 25.13%
Query Match: 4.95%
DB: 7
Length: 355
Matches: 97
Conservative: 45
Mismatch: 88
Indels: 157
Gaps: 14

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Db      24  GlyProThrGln-----GlnArgCysGlyProArgSerLeu-----  35
QY      561  GGTGGGTGCAAGGCGACGATCCTGCGCGCATCATCGGA-----  599
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Db      36  ---GlySer-----ProValLeuGlyLeuAspThrCysValAlaTrp  48
QY      600  -----GATGGCGCCCGCAGTGTCTTGTACGAADAACAATGTATGCCAACGCTG  650
      |||||
Db      49  AspNIwAlaAspGlyGln-----IleLeu  56
QY      651  GGGGAGAAGCCGACCCGTCGTCCGTAAGAC---GAATGTGGGGCCAGTCCGCGCC--ACG  703
      ||::: |||||::: ||| ||||| |||
Db      57  GtGlnLeuAspProLeuThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln  76
QY      704  CAGCGTCCCGCGCATGCCCGCGCGCGCGCGCGGTACTCCACCGAGCGCGCGGCTC  763
      ::: ||| |||||
Db      77  ArgGlyProAlaPheProGly-----MetGlySerGlnGlyLeuArgLeu  91
QY      764  GCGCACTTCAAGGACTGGCCCGAAGACGTAATGCCCAAAACCCGAGAACTGGCAGAGGCC  823
      ||::: ||| ||||| ||||| ||||| ||||| |||||
Db      92  AlAspPheGlyAspTrpProLeuThrAlaGlnValProProGlnLeuLeuAlaAlaAla  111
QY      824  GGAATTCTTATACAGGCCAAGGTGACAAACGAATGCTTCTATTGCGACGAGGGCTA  883
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Db      112  GtYrPhePheNIwThrGlnHISGlnAspValAlaArgCysPhePheCysGlyGlyGlyLeu  131
QY      884  AAGATTTGGAAAGCGATGACGTTCCCTGGGAAACAGACGCGCAGATGTTGACCGCTGC  943
      ::: ||::: ||| ||||| ::: |||||::: ||||| |||||
Db      132  GlnSerTrpLysAlaGlyAspAspProTrpThrGlnHISAlaLysTrpPheProSerCys  151
QY      944  GCGTACGTCGCAATTGGTGAAAGGACGTCATCAATTCAGAAAGTGC-----  988
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Db      152  GlnPheLeuLeuArgSerLysGlyArgAspPheValHISerValGlnGlnThrHISer  171
QY      988  -----  988
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QY      988  -----  988
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Db      232  GlnValGlnAlaAlaArgAspProLeuGlyGlnGlyTrpGlyArgGlyGlyLeuArgAspPro  251
QY      1006  -----  100
Db      252  AspLeuProTrpProIleGlnGlyGlyGlnGlnGlyValGlyThrPheArgArgProVal  271
QY      1007  -----ATATCTGCTAGCGAAGAACAGAGCC-----GCCACCAATGAT  1044
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Db      272  LeuLeuGlyGlyValSerProAlaGlnAlaGlnArgAlaTrpTrpValLeuGlnProPro  291
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Db      292  GtYAlaArgAspValGlnAlaGln--LeuArgArgLeuGlnGlnGlnGlnGlnGlnGlnGln  310
QY      1106  ATATGTTATTCCGAGAGCGTAACGTGTCTTGTGCGCGTGCAGCGTGTGGCGTGC  1166
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Db      311 ValCysLeuAspArgAlaValSerIleValPheValProCysGlyHisLeuVal---Cys 329
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Db      330 AlagluCysAlaProGlyLeuGlnLeuCysProIleCysArgAlaProValArgSerArg 349
QY      1226 GTGCGGCTTACTTCTCG 1243
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RESULT 2
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; Sequence 45, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.1.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-45

Alignment Scores:
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Percent Similarity: 47.46%      Conservative: 21
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Query Match:      3.44%      Indels:      49
DB:              7      Gaps:      9

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QY      501 TCTACTACTCCGTCGCGCGGCGAGCAAGTGTGCTGTCTTCTGTAAAGTAGAATTATGA 560
Db      24 GlyProThrGln-----GluArgCysGlyProArgSerLeu----- 35
QY      561 GGTGGTTCGAAGGCGACGATCTGCGCGCGATCATCGA----- 599
Db      36 ---GlySer-----ProValLeuGlyLeuAspThrCysArgAlaTrp 48
QY      600 -----GATGGGCGCGCCCAAGTGTCCCTTTGTACGAACAATATGTATGCCAAGCTG 650
Db      49 AspHisValAspGlyGln-----IleLeu 56
QY      651 GGGAGAGGCGACCGCTGTCCGTTAGAGAC---GAATGTGGGGCCAGTGCAGCC---ACG 703
Db      57 GlglnLeuArgProLeuThrGlnGluGluGluGluGluGluAlaGlyAlaThrLeuSer 76
QY      704 CAGCTCCCGCGCATGCCCCGCGCGCGGTGCACGCGCGGTACTCCACCGAGCGCGCGGCTC 763
Db      77 ArgGlyProAlaPheProGly-----MetGlySerGluGluLeuArgLeu 91
QY      764 GCCACCTTCAAGACTGCGCGAGACGTATGCGCAAAAACCGAGGAAGTGGCAGAGGCC 823

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QY 764 GCCACCTTCAAGACTGGCCGACGTATGCGCCAAAAACCCAGGAAGCTGGCAGAGCC 823



GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 26, 2005, 16:52:30 ; Search time 269 Seconds
(without alignments)
11720.967 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10041859 @CGN 1 1 408 @runat_23112005_100314_11976 -NCPU=6 -ICPU=3
-NO_MMMap -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	28.2	346	4	US-10-041-859-2 Sequence 2, Appli
2	966	14.4	275	3	US-09-201-936-12. Sequence 12, Appli
3	966	14.4	275	4	US-10-323-643-9. Sequence 9, Appli
4	966	14.4	275	4	US-10-600-272-12. Sequence 12, Appli
5	932.5	13.9	172	4	US-10-041-859-8. Sequence 8, Appli
6	862	12.9	268	4	US-10-323-643-10. Sequence 10, Appli
7	846.5	12.6	172	4	US-10-041-859-10. Sequence 10, Appli
8	831.5	12.4	172	4	US-10-041-859-9. Sequence 9, Appli
9	767.5	11.5	263	5	US-10-706-635-15. Sequence 15, Appli
10	759.5	11.3	172	4	US-10-041-859-11. Sequence 11, Appli
11	719.5	10.8	438	4	US-10-267-502-419. Sequence 419, App

12	719.5	10.8	438	6	US-11-097-143-12366	Sequence 12366, A
13	719.5	10.8	438	6	US-11-097-143-28833	Sequence 28833, A
14	696.5	10.4	172	4	US-10-041-859-12	Sequence 12, Appli
15	554.5	8.3	172	4	US-10-041-859-13	Sequence 13, Appli
16	554.5	7.9	604	4	US-10-232-286-4	Sequence 4, Appli
17	526.5	7.9	604	4	US-10-141-618-6	Sequence 6, Appli
18	526.5	7.9	604	4	US-10-366-307-6	Sequence 6, Appli
19	526.5	7.9	604	4	US-10-730-476A-79	Sequence 79, Appli
20	526.5	7.9	604	5	US-10-825-282-40	Sequence 40, Appli
21	526.5	7.9	604	5	US-10-934-717-4	Sequence 4, Appli
22	526.5	7.9	604	5	US-10-485-225-22	Sequence 22, Appli
23	526.5	7.9	604	5	US-10-730-476A-79	Sequence 79, Appli
24	525.5	7.9	600	3	US-09-974-592-12	Sequence 12, Appli
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26	524.5	7.8	604	3	US-09-974-592-6	Sequence 6, Appli
27	524.5	7.8	604	3	US-09-201-936-6	Sequence 6, Appli
28	524.5	7.8	604	4	US-10-636-065-221	Sequence 221, App
29	524.5	7.8	604	4	US-10-600-272-6	Sequence 40, Appli
30	517.5	7.7	602	3	US-09-201-936-40	Sequence 40, Appli
31	517.5	7.7	602	4	US-10-636-065-227	Sequence 227, App
32	517.5	7.6	602	4	US-10-600-272-40	Sequence 40, Appli
33	507.5	7.6	618	3	US-09-974-592-8	Sequence 8, Appli
34	507.5	7.6	618	3	US-09-201-936-8	Sequence 8, Appli
35	507.5	7.6	618	4	US-10-636-065-223	Sequence 223, App
36	507.5	7.6	618	4	US-10-600-272-8	Sequence 8, Appli
37	500.5	7.5	498	3	US-09-201-936-13	Sequence 13, Appli
38	500.5	7.5	498	4	US-10-600-272-13	Sequence 13, Appli
39	500.5	7.5	618	4	US-10-153-668-338	Sequence 338, App
40	500.5	7.5	618	4	US-10-207-655-200	Sequence 200, App
41	500.5	7.5	618	4	US-10-232-286-2	Sequence 2, Appli
42	500.5	7.5	618	4	US-10-366-307-4	Sequence 4, Appli
43	500.5	7.5	618	4	US-10-361-270-3	Sequence 3, Appli
44	500.5	7.5	618	4	US-10-260-708-63	Sequence 63, Appli
45	500.5	7.5	618	4	US-10-730-476A-78	Sequence 78, Appli

ALIGNMENTS

RESULT 1
US-10-041-859-2
; Sequence 2, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041, 859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260, 478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-041-859-2

Alignment Scores:
Pred. No.: 3 14e-166 Length: 346
Score: 1887.00 Matches: 346
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.20% Indels: 0
DB: 4 Gaps: 0

US-10-041-859A-1 (1-3773) x US-10-041-859-2 (1-346)

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QY 266 GCGCGGATGC AAAATGCGACCTTTCATTTGGTCCGCTCATGTTATCCTCGTGAAGTCT 325
Db 21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
QY 326 TCAACGACATCCACACTCCCGTCACCTTTCGTGCTGACGTGATAAACGATTAATCAGCAC 385
Db 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60
QY 386 ACATTCAACTTCCTTCCTGATATGCCCCGACATGCGCTGTGAAGAGAAAGTGTGAACA 445
Db 61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluValArgLeuLysThr 80
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Db 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100
QY 506 TACCTCGGTCCGGCGGCGAAGTGTGCTGTGCTTTCTGTAAAGTAGAAATTATGAGGTGG 565
Db 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrp 120
QY 566 GTCGAAGCGCAGCATCTGCCCCGATCATCGAGATGGCGCCCGCCAGTGTCCCTTTGTA 625
Db 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140
QY 626 CGAAACAATGTATGCGCAACGCTGGGGAGAGAGCGCACCGCTGTGCTAGAGACGAATGT 685
Db 141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160
QY 686 GGGGCCAGTGGCGGCACGAGCCCTCCCGCATGCCCCGCGCCCGTGACGCGCGGTACTCC 745
Db 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
QY 746 ACCGAGCGCGCGCTGCGCCACCTTCAAGACTGGCGCGAAGACTGATGCGCCCAAAACCC 805
Db 181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgMetArgGlnLysPro 200
QY 806 GAGGAACCTGGCAGAGCGCGGATTCTTCTATACAGGCCAAGGTGACAAAACGAATGCTTC 865
Db 201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220
QY 866 TATTGCGACGAGGGCTAAAGATTGGAAAGCGATGACGTTCCGTGGAAACGACGCGC 925
Db 221 TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
QY 926 AGATGTTGACCGCGCTGCGCGTACGTGCAATTGGTGAAGAGCAGTACTACATTCAAGA 985
Db 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys 260
QY 986 GTGAAGTCGAGGGCCACTGCGATATCTGCTAGCCGAAGAAGAACAGGCGCCCAATGAT 1045
Db 261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGlnGluAlaAlaThrAsnAsp 280
QY 1046 TCGACTAAGAACGTCCGCCAAGAGGGCGAAGAAACATTGGATGACTTAAATATGTAAA 1105
Db 281 SerThrLysAsnValaIaGlnGluGlyLysHisLeuAspAspSerLysIleCysLys 300
QY 1106 ATATGTTATTCGAGGAGCGTAACGTGTGCTTTCGTGCGCGTGCAGGACGTTGCGCTGC 1165
Db 301 IleCysTyrSerGluValArgAsnValCysPheValProCysGlyHisValAlaCys 320
QY 1166 GCCAAGTGGCGCTGTGACGAGCAAGTGCCTGCTGCTGCGCAGGACGTTCAAGATGCG 1225
Db 321 AlaLysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAla 340
QY 1226 GTGCGGCTTACTTCTCG 1243
Db 341 ValArgLeuTyrPheSer 346

RESULT 2
US-09-201-936-12

; Sequence 12, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 275
; TYPE: PRN
; ORGANISM: Cydia pomonella
US-09-201-936-12

Alignment Scores:
Pred. No.: 1.54e-80 Length: 275
Score: 966.00 Matches: 171
Percent Similarity: 72.66% Conservative: 39
Best Local Similarity: 59.17% Mismatches: 55
Query Match: 14.44% Indels: 24
DB: 3 Gaps: 3

US-10-041-859A-1 (1-3773) x US-09-201-936-12 (1-275)

QY 407 ATGCCGACATGCGTCTGAAGAGAAAGTCTGAACAATTTGATCAGTGCCGCTTACG 466
Db 1 MetSerAspLeuArgLeuGluGluValArgLeuAsnThrPheGluLysTrpProValSer 20
QY 467 TTTTGCACGCCGGAACAATTGGCCCCGCAACGATTTCTACTACCTCGGTGCGCGCAGAA 526
Db 21 PheLeuSerProGluThrMetAlaLysAsnGlyPheTyrTyrLeuGlyArgSerAspGlu 40
QY 527 GTGTGCTGTCTTCTGTAAAGTTAGAAATTAGGTGGGTGGAAGCGCAGATCCTGCC 586
Db 41 ValArgCysAlaPheCysLysValGluIleMetArgTrpLysGluGlyGluAspProAla 60
QY 587 GCCGATCATCGAGATGGCGCCCGCCAGTGTCCCTTTGTACGAAAACAATGTATGCCAAC 646
Db 61 AlaAspHisLysValTrpAlaProGlnCysProPheValLys----- 74
QY 647 GCTGGGGAGAGCGCACCGCTGCTGAGACGAATGTGGGGCCAGTGGCCACGACGAG 706
Db 75 -----GlyIleAspValCysGlySerIleValThrThrAsn 86
QY 707 -----CCTCCCGCATGCCCGCGCCCGCCCGTGCACGCGCGTACTCC 745
Db 87 AsnIleGlnAsnThrThrThrHisAspThrIleIleGlyProAlaHisProLysTyrAla 106
QY 746 ACCGAGCGCGCGCGCTCGCCACCTTCAAGACTGCGCGAGACGTAATGCGCAAAACCC 805
Db 107 HisGluAlaAlaArgValLysSerPheHisAsnTrpProArgCysMetLysGlnArgPro 126
QY 806 GAGGAACGTGACAGAGCGCGATTCTTCTAATACAGCGCAAGGTGACAAAAGAAATGCTTC 865
Db 127 GluGlnMetAlaAspAlaGlyPhePheTyrThrGlyTyrGlyAspAsnThrLysCysPhe 146
QY 866 TATTGCGACGAGGGCTAAAGATTGGAAAGCATGACGTTCCGTGGGAAACAGACGCGC 925
Db 147 TyrCysAspGlyGlyLeuLysAspTrpGluProGluAspValProTrpGluGlnHisVal 166

Db 12 LylLysSerGlyLeuGlnMetAspIleThrIlyValAlaSerAenglySerSerSerThr 31

QY 248 TTGGTGATGTTAAAAAT---GCCGGGATGCAAAAATGGCACTTTCATTGGTCCGCTC 304

Db 32 LeuThrLeuPheLysSerGlySerLeuGlnAlaLysIleArgPro--LeuAlaProLeu 50

QY 305 ATGTTA-----TCCTCGTGTAGTCTTCAACGACATCCACACTCCCGTCACCTTCGTCG 358

Db 51 MetLeuProThrProSerTyrAspSerAsnAlaGlySerProSerLeuSerProSerThr 70

QY 359 -----TCAGCTGATAAAACGGATTAATCACGACACATTCACCTTC 397

Db 71 ProCysSerSerSerSerPheSerIleAspIlyThrAspAsnHisAspThrPheGlyPhe 90

QY 398 CTTCCCTGATATGCCGACATGCGTCGTGAAGAGAAAGCTGAAAAACATTGTGATCAGTGG 457

Db 91 SerAlaAspThrValAspMetArgLysGlnAspGlnArgMetLysThrPheGlnLysIle 110

QY 458 CCGGTTACGTTTGTGACGCGCGGAACAATTGGCCCGCAACGGATTCTACTACCTCGGTCCG 517

Db 111 ProValSerPheLeuSerGlyGlnGlnLeuAlaArgAsnGlyPheTyrIleuGlyArg 130

QY 518 GCGGACGAAGTGTGCTGTCTTCTGTAAAGTAGAAATTATGAGGTGGGTCCGAGCGGAC 577

Db 131 ArgAspGlnAlaArgCysAlaPheCysLysValGlnIleMetArgTrpValGlnGlyAsp 150

QY 578 GATCCTGCGCGGATCATCGAGATGGCGCGCCAGTCCCTTTGTACGAAAACAATG 637

Db 151 AspProAlaLysAspHisGlnArgTrpAlaProGlnCysProPheValArgLys--Leu 169

QY 638 TATGCCAACGCTGGGGAGAGGACGCGCTGCTGCTAGAGACGAATGTGGGCGCAGTGC 697

Db 170 AenglyThrAlaAlaAspThrGlySerSerGlyGlnAspGlnCysGlyAlaArgAla 189

QY 698 GCC-----ACGACGCTCCCGCATGCCCCGCGCGCGCGGCTACTCCACC 748

Db 190 AlaProSerGlyThrSerProProArgMetAlaGlyProValHisProArgTyrAlaSer 209

QY 749 GAGGCGCGCGGCTCGCCCACTTCAAGGACTGGCGCGGACGATATGCGCCAAAAACCCGAG 808

Db 210 GlnAlaAlaArgLeuArgSerPheLysAspTrpProArgCysMetArgGlnLysProGln 229

QY 809 GAACTGGCAGAGGCGCGGATTTCTTATACAGGCGCAAGGTGACAAAAAGAAATGCTTCTAT 868

Db 230 GlnLeuAlaGlnAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPheTyr 249

QY 869 TCGGACGGAGGGCTAAAGATTGGGAAAGCGATGACGTTCCGTGGGAACAGACGCCAGA 928

Db 250 CysAspGlyGlyLeuLysAspTrpGlnAsnHisAspValProTrpGlnGlnHisAlaArg 269

QY 929 TGGTTGACCGCTGCGCGCTACGTCGAATTGGTGAAGGACGTCGACTACATTGACAGAGGTG 988

Db 270 TrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgGlnTyrValGlnLysVal 289

QY 989 AAGTCGGAGGCCACTGCGATATCTGTAGCGAAGAAACAG-----GCCGCCACC 1039

Db 290 IleSerGlnAlaCysGlnValSerAlaSerGlnAlaGlnArgAspValAlaProAlaArg 309

QY 1040 AATGATTGCACTAAGAACGTCGCCCAAGAGGGCGGAAACATTGGATGACTTAAATA 1099

Db 310 ThrAlaGlnProSerProProAlaGlnAlaProGlnAsnSerValAspAspSerLysLeu 329

QY 1100 TGTAAATATGTATTCTCGAGGAGCGTAACGTGTGCTTGTGCGCGCGGCGCAGTGGTG 1159

Db 330 CysLysIleCysTyrAlaGlnGlnArgAsnValCysPheValProCysGlyHisValVal 349

QY 1160 GCGTGGCCCAAGTGGCGGCTGTGACGAGCAACAAGTCCGATGTGTGCAGAGCTTCACG 1219

Db 350 AlaCysAlaLysCysAlaLeuAlaAlaAspLysCysPrometCysArgArgThrPheGln 369

QY 1220 AATGCGGTGCGGCTTACTTCTCG 1243

Db 370 AsnAlaValArgLeuTyrPheSer 377

RESULT 2

US-08-511-485-12

; Sequence 12, Application US/08511485

; Patent No. 5919912

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.

; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

; TITLE OF INVENTION: PROBES, AND DETECTION METHODS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/511,485

; FILING DATE: 04-AUG-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 07540/002001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 275 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: both

; MOLECULE TYPE: protein

US-08-511-485-12

Alignment Scores:

Pred. No.:	7.45e-95	Length:	275
Score:	966.00	Matches:	171
Percent Similarity:	72.66%	Conservative:	39
Best Local Similarity:	59.17%	Mismatches:	55
Query Match:	14.44%	Indels:	24
DB:	1	Gaps:	3

US-10-041-859A-1 (1-3773) x US-08-511-485-12 (1-275)

QY 407 ATGCCGACATGCGTCGTGAAGAGGAACGTCGAAAAACATTGTGATGAGTGGCCGTTACG 466

Db 1 MetSerAspLeuArgLeuGlnGlnValArgLeuAsnThrPheGlnLysTrpProValSer 20

QY 467 TTTTGACGCGCGGAAACAATTGGCCCGCAACGGATTCTACTACCTCGGTCCGGCGAGGAA 526

Db 21 PheLeuSerProGlnThrMetAlaLysAsnGlyPheTyrIleuGlyArgSerAspGln 40

QY 527 GTGTGCTGTGCTTTCTGTAAAGTAGAAATTATGAGGTGGGTGGAAGCGGACGATCTGCC 586

Db 41 ValArgCysAlaPheCysLysValGlnIleMetArgTrpLysGlnGlyGlnAspProAla 60

QY 587 GCCGATCATCGAGATGGCGCGCCAGTGTCCCTTTGTACGAAAAACAATGTATGCCAAC 646

Db 61 AlaAspHisLysLysValTrpAlaProGlnCysProPheValLys----- 74

QY 647 GCTGGGGAAGCGGACCGGCTGTGCGTGAAGACGAATGTGGGCGGCGGCGCACGAG 706

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 26, 2005, 15:36:38 ; Search time 430.5 Seconds
(without alignments)
12366.821 Million cell updates/sec

Title: US-10-041-859A-1

Perfect score: 6692

Sequence: 1 cattactaacctcacttcac.....tcgcgctctactctcgtga 3773

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US10041859/runat_23112005.100312.11856/app_query.fasta_1.3911
-DB=UniProt -QFMT=faстан -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10041859 @CGN 1_1_689 @runat_23112005.100312.11856 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	28.2	346	2	Q968T8_BOMMO
2	1866	27.9	346	2	Q81S31_BOMMO
3	1333.5	19.9	379	2	Q9U492_TRINI
4	1319	19.7	377	2	Q9NU07_SPOFR
5	966	14.4	275	1	IAP_GVCP
6	937	14.0	287	2	Q6E7G7_NPVAG
7	890.5	13.3	280	2	Q6VTV9_NPVCD
8	879	13.1	263	2	Q80SF4_NPVHC
9	876	13.1	281	2	Q9YNI8_NPVCF
10	873	13.0	261	2	Q9QES9_NPVBP
11	873	13.0	276	2	Q89744_NPVBS
12	862	12.9	268	1	IAP3_NPVOP
13	782	11.7	264	2	Q9EN27_AMEPV
14	747.5	11.2	255	2	Q7T5S1_GVCL
15	728	10.9	313	2	Q9J827_9NUCL
16	719.5	10.8	438	1	IAP1_DROME

17	701	10.5	403	2	Q8WRD9_AEDTR	Q8wrds aedes trise
18	684	10.2	401	2	Q6Q507_AEDAE	Q6q507 aedes aegyp
19	676.5	10.1	402	2	Q8T621_AEDAL	Q8t621 aedes albop
20	662	9.9	285	2	Q8JM16_9NUCL	Q8jml6 mamestra co
21	653	9.8	276	2	Q7IA73_9NUCL	Q7ia73 mamestra co
22	653	9.8	276	2	Q8QL95_NPVMC	Q8ql95 mamestra co
23	635	9.5	283	2	Q80LK8_NPVAH	Q80lk8 adoxophyes
24	623.5	9.3	278	2	Q4KT41_9NUCL	Q4kt41 chrysodeixi
25	573	8.6	254	2	Q7T9S6_GVAO	Q7t9s6 adoxophyes
26	550	8.2	414	2	Q4T660_TETNG	Q4t660 tetraodon n
27	544.5	8.1	269	2	Q6QXJ6_GVAS	Q6qxj6 agrotis seg
28	542	8.1	358	1	PIAP_PIG	Q62640 sus scrofa
29	538.5	8.0	304	2	Q5TWU6_ANOGA	Q5twu6 anopheles g
30	532.5	8.0	268	2	Q9E232_9NUCL	Q9e232 hellicoverpa
31	530.5	7.9	401	2	Q8JHV9_XENLA	Q8jlv9 xenopus lae
32	530	7.9	186	2	Q7QJ55_ANOGA	Q7qj55 anopheles g
33	529.5	7.9	268	2	Q7TLM6_9NUCL	Q77lm6 hellicoverpa
34	529.5	7.9	268	2	Q9IFI8_9NUCL	Q9ifi8 hellicoverpa
35	528.5	7.9	602	2	Q9ESE9_RAT	Q9ese9 rattus norv
36	528.5	7.9	602	2	Q5XIW4_RAT	Q5xiw4 rattus norv
37	526.5	7.9	604	1	BIRC3_HUMAN	Q13489 homo sapien
38	526	7.9	604	2	Q6DDYJ_XENLA	Q6ddyj xenopus lae
39	525.5	7.9	600	1	BIRC3_MOUSE	Q08863 mus musculu
40	522	7.8	604	2	Q6GLD7_XENTR	Q6glld7 xenopus tro
41	516.5	7.7	616	2	Q8Q4E2 ICTPU	Q804e2 ictalurus p
42	514	7.7	628	2	Q8UWD2_BRARE	Q8uwd2 brachydanio
43	514	7.7	647	2	Q7TOK2_BRARE	Q7tok2 brachydanio
44	514	7.7	654	2	Q6ZM93_BRARE	Q6zm93 brachydanio
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ALIGNMENTS

RESULT 1
Q968T8_BOMMO Q968T8_BOMMO PRELIMINARY; PRT; 346 AA.
ID Q968T8; AC Q968T8;
AC Q968T8; DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=IAP;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21240184; Pubmed=11341966; DOI=10.1016/S0167-4889(00)00105-1;
RA Huang Q., Deveraux Q.L., Maeda S., Stennicke H.R., Hammock B.D.,
RA Reed J.C.;
RT "Cloning and characterization of an inhibitor of apoptosis protein
(IAP) from Bombyx mori.";
RT Biochim. Biophys. Acta 1499:191-198(2001).
RL EMBL; AF281073; AAK57560.1; -; mRNA.
DR HSSP; Q24306; 1Q4Q.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_I32_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM0184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38942 MW; 6CFC6C6468894C69 CRC64;

Alignment Scores:

Pred. No.: 3.29e-155 Length: 346
Score: 1887.00 Matches: 346
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.20% Indels: 0
DB: 2 Gaps: 0

US-10-041-859A-1 (1-3773) x Q968T8_BOMMO (1-346)

QY 206 ATGAGTTGACGAAAGTTGCTAAAAATGAGCTGCCGCCACGTTGGTATGTTAAAAAT 265
Db 1 MetGluLeuThrIysValAlaIysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20
QY 266 GCGCGGATGC AAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGAAGTCT 325
Db 21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
QY 326 TCAACGACATCCACACTCCCGCTCACCTTCGTCTGCTAGCTATAAACGGATTAATCAGC 385
Db 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60
QY 436 ACATTCAACTTCCTTCGTATATGCCGACATGCGCTGTGAAGAGAAGACGCTGAAAAA 445
Db 61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluValArgLeuLysThr 80
QY 446 TTTGATCAGTGCGCCGTTACGTTTTTGACGCGCGGAACAATTGGCCCCGCAACGATTCTAC 505
Db 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100
QY 506 TACCTCGTCCGCGCGACGAAGTGTGCTGTCTTCTGTAAAGGTAGAATTTATGAGTGG 565
Db 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrp 120
QY 566 GTCGAAGCGCAGCATCTCTGCCCGCCGATCATCGAGATGGGCGCCCGCAGTGTCCCTTTGTA 625
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QY 626 CGAAAAACAATGTATGCCAACGCTGGGGAGAGGCGACCGCTGTGCTAGAGACGAATGT 685
Db 141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160
QY 686 GGGGCCAGTGGCGGCCACAGCCTCCCGCATGCCCGGCCCGCCGTGCACGCGCGTACTCC 745
Db 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
QY 746 ACCGAGCGCGCGCGCTCCGCCACCTTCAAGGACTGGCGCGAGACGTATGCCCAAAACC 805
Db 181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgMetArgGlnLysPro 200
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Db 201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220
QY 866 TATTGCGACGAGGGGCTAAAGATTGGAAAGCGATGACGTTCCGTGGAAACAGCAGCC 925
Db 221 TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
QY 926 AGATGTTGACCGCTGCCGTACGTCGAATTGGTGAAGAGCGTACTATCAATTCAGAA 985
Db 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys 260
QY 986 GTGAAGTCGAGGCGCACTGCCATATCTGCTAGCGAAGAAGACAGGCGCGCAACATGAT 1045
Db 261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGlnAlaAlaThrAsnAsp 280
QY 1046 TCGACTAAGAACGTCGCCCAAGAGGGCGAAGAACATTTGGATGACTCTAAATAATGTA 1105
Db 281 SerThrLysAsnValAlaGlnGluGlyGluLysHisLeuAspAspSerLysIleCysLys 300
QY 1106 ATATGTTATTCGAGGAGCGTAAAGTGTGCTTCGCGCGTGCAGCGCACGTGGTGGCGTGC 1165
Db 301 IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValAlaCys 320

QY 1166 GCCAAGTGGCGCTGTGACGAGACAGTAGTCCCGATGTGTCCGACAGACGTTACGAATGCG 1225
Db 321 AlaLysCysAlaLeuSerThrAspLysCysPrometCysArgArgThrPheThrAsnAla 340
QY 1226 GTGCGGCTCTACTTCTCG 1243
Db 341 ValArgLeuTyrPheSer 346

RESULT 2
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ID Q8IS31_BOMMO PRELIMINARY; PRT; 346 AA.
AC Q8IS31_
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang G., Wang L., Wu X.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY155274; AAN46550.1; -; mRNA.
DR HSSP; Q24306; 104Q.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_132_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38849 MW; 5450EB75F56A8486 CRC64;

Alignment Scores:
Pred. No.: 2.22e-153 Length: 346
Score: 1866.00 Matches: 343
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 3
Query Match: 27.88% Indels: 0
DB: 2 Gaps: 0

US-10-041-859A-1 (1-3773) x Q8IS31_BOMMO (1-346)

QY 206 ATGAGTTGACGAAAGTTGCTAAAAATGAGCTGCCGCCACGTTGGTATGTTAAAAAT 265
Db 1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaAlaThrLeuValMetLeuLysAsn 20
QY 266 GCGCGGATGC AAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGAAGTCT 325
Db 21 AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
QY 326 TCAACGACATCCACACTCCCGCTCACCTTCGTCTCAGCTGATATAAACGGATTAATCAGC 385
Db 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60
QY 386 ACATTCAACTTCCTTCGTATATGCCGACATGCGCTGTGAAGAGAAGACGCTGAAAAA 445
Db 61 ThrPheAsnPheLeuProAspMetProAspMetArgArgGluGluValArgLeuLysThr 80
QY 446 TTTGATCAGTGCGCCGTTACGTTTTTGACGCGCGGAACAATTTGGCGCGCAACGATTTCTAC 505
Db 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100
QY 506 TACCTCGTCCGCGCGACGAAGTGTGCTGTCTTCTGTAAAGGTAGAATAATTAGAGTGG 565

Db	41	ValArgCysValApheCysValysValGluIleMetArgTrpLysGluGlyGluAspProAla	60
QY	587	GCCGATCATCGAGATGGCGCCGCCAGTGTCCCTTGTACGAAACAAATGTATGCCAAC	646
Db	61	AlaAspHisbLysbLysTrpAlaProGlnCysbProPheValLys-----	74
QY	647	GCTGGGGAGAGCCGCGCTGTCCGTAGAGACGAATGTGGGGCCAGTGGCGCCAGCAG	706
Db	75	-----GlyIleAspValCysbGlySerileValThrThrAsn	86
QY	707	-----CCTCCCGCATGCCGCGCCCGGTGCACGCGCGGTACTCC	745
Db	87	AsnIleGlnAsnThrThrThrHisAspThrIleIleGlyProAlaHisProLysTyAla	106
QY	746	ACCGAGCCGCGCGCTGCCACCTTCAAGACTGGCCGAGACGTATGCGCAAAACCC	805
Db	107	HisGluAlaAlaArgValLysSerPheHisAsnTrpRoArgCysMetLysGlnArgPro	126
QY	806	GAGGAAGTGCAGAGCGCGGATCTCTATATACAGGCCAAGGTGACAAACGAATGCTTC	865
Db	127	GluGlnMetAlaAspAlaGlyPhePheTyrThrGlyTyArgAspAsnThrLysCysPhe	146
QY	866	TATTGCGACGGAGGCTTAAAGATTGGGAAAGCCGATGACGTTCCGTGGGAACAGCAGCC	925
Db	147	TyrCysAspGlyGlyLeuLysAspTrpGluProGluAspValProTrpGluGlnHisVal	166
QY	926	AGATGTTTCGACCGCTGCGCGGTACGTGCAATTGGTGAAGGACGTGACTACATTCAGAG	985
Db	167	ArgTrpPheAspArgCysValaTyArgValGlnLeuValLysGlyArgAspTyArgValGlnLys	186
QY	986	GTGAAGTCGAGGCCACTGCGATA-----TCTGCTAGCGAAGAGAAGACAGCGCCGC	1036
Db	187	ValIleThrGluAlaCysValLeuProGlyGluAsnThrThrValSerThrAlaAlaPro	206
QY	1037	ACCAATGATTCGACGTAGAAGCTGCCCAAGAGGCGGAGAAACATTTGGATGACTCTAA	1096
Db	207	ValSerGluProIleProGluThrLysIleGlyLysGluProGlnValGluAspSerLys	226
QY	1097	ATATGTAATAATATGTATTCCGAGAGCGGTACGTTGCTTCGTGCCGTGGCCACGTTG	1156
Db	227	LeuCysLysIleCysbTyArgValGluGluCysbIleValCysbPheValProCysbGlyHisVal	246
QY	1157	GTGCGGTGCGCAAGTGGCGGCTGTGCAGCGGACAGTCCGATGTGTGCGAGGACGTTTC	1216
Db	247	ValAlaCysAlaLysCysAlaLeuSerValAspLysCysbPrometCysArgLysIleVal	266
QY	1217	ACGAATGCGGTGCGGCTCTACTTCTCG	1243
Db	267	ThrSerValLeuLysValTyrPheSer	275

RESULT 2
T10304
inhibitor of apoptosis protein 3 - Orgyia pseudotsugata nuclear polyhedrosis virus
C/Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMPV
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2000
C/Accession: T10304
R/Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virol. 229, 381-399, 1997
A/Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A/Reference number: Z17011; MUID:97271300; PMID:9126251
A/Accession: T10304
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-268 <AHR>
A/Cross-references: UNIPARC:UPI00006180F; EMBL:U75930; NID:g2934903; PIDN:AAC59034.1; F
C/Superfamily: viral apoptosis inhibitor IAP; RING finger homology
F;217-261/Domain: RING finger homology <RRN>

Alignment Scores:
Pred. No.: 2.98e-66 Length: 268
Score: 862.00 Matches: 150
Percent Similarity: 65.82% Conservative: 31
Best Local Similarity: 54.55% Mismatches: 72

Query Match:	12.88%	Indels:	22
DB:	2	Gaps:	2
US-10-041-859A-1 (1-3773) x T10304 (1-268)			
QY	413	GACATGCGTGTGAAGAGGAACGTCTGMAAATTTGATCATGTGCCCCGTTTACGTTTGG	472
Db	14	AspMetLysAsnLysAlaAlaArgLeuGlyThrTyrThrAsnTrpProValGlnPheLeu	33
QY	473	ACGCCGAACAATTGGCCCCGCAACGATTTCTACTCCTCGGTGCGCGCGCAAGTGTGC	532
Db	34	GluProSerArgMetAlaAlaSerGlyPheTyrTrpLeuGlyArgGlyAspGluValArg	53
QY	533	TGTGCTTCTGTAAAGTGAATATATGAGGTGGTCCGAAGCCGATCTGCCCGCAT	592
Db	54	CysAlaPheCysLysValGluIleThrAsnTrpValArgGlyAspAspProGluThrAsp	73
QY	593	CATCGGAGATGGCGCCCCAGTGTCCCTTTGTACGAAACAAATGTATGCGCAACGCTGGG	652
Db	74	HisLysArgTrpAlaProGlnCysbProPheValArgAsnAsnAlaHisAspThrProHis	93
QY	653	GGAAGCGGACCGCTGTCCGTAGAGACGAATGTGGGCCAGTGGCCAGCAGCTCCC	712
Db	94	AspArgAla-----ProPro	98
QY	713	CGCATGCCGCGCCGTGCACGCGCGGTACTCCACCGAGCGCGCGCTGCCACCTTC	772
Db	99	AlaArgSerAlaAlaAlaHisProGlnTyAlaThrGluAlaAlaArgLeuArgThrPhe	118
QY	773	AAGGACTGGCCGACGTAATGCGCCAAACCCGAGAACTGGCAGAGCCGGATTCTTC	832
Db	119	AlaGluTrpProArgGlyLeuLysGlnArgbProGluLeuAlaGluAlaGlyPhePhe	138
QY	833	TATACAGGCCAAGGTGACAAACGAATGCTTCTATTGCGAGCGAGGGCTTAAAGATTGG	892
Db	139	TyrThrGlyGlnGlyAspLysThrArgCysbPheCysCysAspGlyGlyLeuLysAspTrp	158
QY	893	GAAGCGATGACGTTCCGTGGGAACAGCAGCCAGATGGTTGCAACCGCTGCGGTACGTG	952
Db	159	GluProAspAspAlaProTrpGlnGlnHisAlaArgTrpTyArgAspArgCysGluTyArgVal	178
QY	953	CAATTGTTGAAGAGCTGACTACATTCAGAAGTGAAGTCGAGGCCACTGCGATATCT	1012
Db	179	LeuLeuValLysGlyArgAspPheValGlnArgValMetThrGluAlaCysValValArg	198
QY	1013	GCTAGCGAAGAGAACAGGCCGCCCAATGATTCGACTAAGACGTCGCCCAAGAGGGC	1072
Db	199	AspAlaAspAsnGluProHisIleGluArgProAlaVal-----	211
QY	1073	GAGAAACATTTGATGACTCTAAATATGTAAATATGTATTCCGAGAGCGTTAACGTG	1132
Db	212	GluAlaGluValAlaAspAspArgLeuCysbLysIleCysbLeuGlyAlaGlyLysThrVal	231
QY	1133	TGCTTCGTGCGGTGCGGCCACGTTGTTGGCGCCCAAGTGCAGCTGCGGTGAGCAAG	1192
Db	232	CysbPheValProCysbGlyHisValValAlaCysbGlyLysCysAlaAlaGlyValThrThr	251
QY	1193	TGCCCGATGTGTGCGAGACGTTACAGAAAGCGGTGCGGCTCTAC	1237
Db	252	CysbProValCysArgGlyGlnLeuAspLysAlaValArgMetTyr	266

RESULT 3
A53989
apoptosis-inhibiting protein - Orgyia pseudotsugata multicapsid nuclear polyhedrosis viru
C/Species: Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus, OpMPV
C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C/Accession: A53989
R/Birnbaum, M.J.; Clem, R.J.; Miller, L.K.
J. Virol. 68, 2521-2528, 1994
A/Title: An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polype
A/Reference number: A53989; MUID:94187094; PMID:8139034
A/Accession: A53989
A/Status: preliminary

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 26, 2005, 10:20:33 ; Search time 289.5 Seconds
(without alignments)
11452.685 Million cell updates/sec

Title: US-10-041-859A-1
Perfect score: 6692
Sequence: 1 cattattaactcacttcac.....tcgcgctctactctctgtga 3773

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US10041859/runat_23112005.100311.11846/app_query.fasta_1.3911
-DB=A_Geneseq -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10041859_@CGN_1_1.429_@runat_23112005.100311.11846 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1887	28.2	346	5	ABB78046	Abb78046 Amino aci
2	1319	19.7	377	4	AAE07881	Aae07881 Fall army
3	767.5	11.5	263	5	ABB09488	Abb09488 AMEPV bac
4	721.5	10.8	438	4	AAB48189	Aab48189 Drosophil
5	719.5	10.8	438	4	ABB61858	Abb61858 Drosophil
6	719.5	10.8	438	4	ABB67347	Abb67347 Drosophil
7	719.5	10.8	438	4	AAB48188	Aab48188 Drosophil
8	719.5	10.8	438	4	AAB48190	Aab48190 Drosophil
9	719.5	10.8	438	8	ADO08093	Ado08093 Fly polyp

10	713.5	10.7	438	4	AAB48192	Aab48192 Drosophil
11	713.5	10.7	438	4	AAB48191	Aab48191 Drosophil
12	711.5	10.6	438	4	AAB48196	Aab48196 Drosophil
13	709.5	10.6	438	4	AAB48197	Aab48197 Drosophil
14	708.5	10.6	438	4	AAB48193	Aab48193 Drosophil
15	708.5	10.6	438	4	AAB48194	Aab48194 Drosophil
16	576.5	8.6	434	4	AAB48195	Aab48195 Drosophil
17	526.5	7.9	604	2	AAW19747	Aaw19747 Human inh
18	526.5	7.9	604	2	AAW13546	Aaw13546 Human c-I
19	526.5	7.9	604	2	AAV52703	Aay52703 Human cel
20	526.5	7.9	604	2	AAV33997	Aay33997 Human cel
21	526.5	7.9	604	6	ABU07431	Abu07431 Protein d
22	526.5	7.9	604	6	ABB82739	Abb82739 Human CIA
23	526.5	7.9	604	7	ADB80948	Adb80948 RING-SH c
24	526.5	7.9	604	7	AAE39811	Aae39811 Human cel
25	526.5	7.9	604	8	ADG87135	Adg87135 Human CIA
26	526.5	7.9	604	8	ADH74643	Adh74643 Human CIA
27	526.5	7.9	604	8	ADS88171	Ads88171 Human pro
28	526.5	7.9	604	8	ADR89114	Adr89114 Human IAP
29	526.5	7.9	604	8	ADR67238	Adr67238 Human bla
30	526.5	7.9	604	8	ADU22899	Adu22899 Human apo
31	525.5	7.9	600	2	AAW69298	Aaw69298 Murine HI
32	525.5	7.9	600	6	ABP72155	Abp72155 Mouse inh
33	524.5	7.8	604	2	AAW19582	Aaw19582 Human apo
34	524.5	7.8	604	2	AAW69295	Aaw69295 Human HIA
35	524.5	7.8	604	5	ABG65664	Abg65664 Human inh
36	517.5	7.7	602	5	ABG65667	Abg65667 Mouse inh
37	516.5	7.7	602	2	AAW19585	Aaw19585 Mouse apo
38	507.5	7.6	618	2	AAW19583	Aaw19583 Human inh
39	507.5	7.6	618	2	AAW69296	Aaw69296 Human HIA
40	507.5	7.6	618	5	ABG65665	Abg65665 Human inh
41	501	7.5	497	7	ADI39803	Adi39803 Drosophil
42	500.5	7.5	496	2	AAW19745	Aaw19745 Mouse inh
43	500.5	7.5	618	2	AAW19746	Aaw19746 Human inh
44	500.5	7.5	618	2	AAW13545	Aaw13545 Human c-I
45	500.5	7.5	618	2	AAV33998	Aay33998 Human cel

ALIGNMENTS

RESULT 1	
ID	ABB78046
AC	ABB78046 standard; protein; 346 AA.
XX	
AC	ABB78046;
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	Amino acid sequence of inhibitor of apoptosis protein BmiAP.
XX	
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;
KW	Spodoptera frugiperda; insult-resistant plant; caspase.
XX	
OS	Bombyx mori.
XX	
FH	Key
FT	Domain
FT	74..140
FT	/note= "BIR domain 1"
FT	182..249
FT	/note= "BIR domain 2"
FT	298..314
FT	/note= "RING domain"
XX	
PN	WO200253586-A2.
XX	
PD	11-JUL-2002.
XX	
PF	07-JAN-2002; 2002WO-US000314.
XX	
PR	08-JAN-2001; 2001US-0260478P.
XX	
PA	(BURN-) BURNHAM INST.
XX	

PI Maeda S, Huang Q, Reed JC, Devereux QL;
XX WPI; 2002-590628/63.
DR N-PSDB; ABQ78228.
XX
PT Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT apoptosis and identifying an agent that modulates activity of
PT polypeptide.
XX
PS Claim 39; Page 31; 62pp; English.
XX
CC The present score represents a polypeptide which is an inhibitor of
CC apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is
CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC mori cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insult-resistant plant. BmiAP is also
CC useful for inhibiting caspases
XX
SQ Sequence 346 AA;

Alignment Scores:
Pred. No.: 3.32e-182 Length: 346
Score: 1887.00 Matches: 346
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.20% Indels: 0
DB: 5 Gaps: 0

US-10-041-859A-1 (1-3773) x ABB78046 (1-346)

QY 206 ATGAGTTGACGAAAGTGGCTAAATAATGAGCTGCCGCCACGTTGGTATGTTAAATAAT 265
DB 1 MetGluLeuThrIysValAlaIysAsnGlyAlaAlaThrLeuValMetLeuIysAsn 20
QY 266 GCGCGGGATGCAGAAATGCGACCTTTCATGTGTCGCTCATGTTATCCTCGTGGAGTCT 325
DB 21 AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
QY 326 TCAACGACATCCACACTCCCGTCACTTCGTGCTGCTAGCTGATTAACGATATACGAC 385
DB 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp 60
QY 386 ACATTCAACTTCCTTCGATATGCCCCGACATGCGTCGTGAAGAGAAAGCTGAAACA 445
DB 61 ThrPheAsnPhelLeuProAspMetProAspMetArgArgGluGluIuArgLeuLysThr 80
QY 446 TTTGATCAGTGGCCCGTTACGTTTGTGACGCCGGAACAATTGGCCCCGACGATTTCTAC 505
DB 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100
QY 506 TACCTCGTCCGCGCGACGAAAGTGTGCTGTGCTTCTGTTAAGGTAGAAATTATGAGTGG 565
DB 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrp 120
QY 566 GTCGAAGCGGACGATCTGCCCGCATCATCGAGATGGCGCCCCAGTGTCCCTTTGTA 625
DB 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140
QY 626 CGAAACAAATGTATGCGCAACGCTGGGAGAGAGCGCGCTGTCGTTAGAGACGAATGT 685
DB 141 ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValAlaGlyArgAspGluCys 160
QY 686 GGGCCAGTGGCGCGCACGAGCCTCCCGCATGCGCGGCGCCCGTGACGCGGTAATCC 745
DB 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
QY 746 ACCGAGCGCGCGGCTCGCCACCTTCAAGGACTGGCCGAGACGTATGCGCCAAAAACC 805
DB 181 ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro 200

QY 806 GAGAACTGGCAGAGCCGGATTCTTCTATACAGCCCAAGGTGACAAAAAGAAATGCTTC 865
DB 201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe 220
QY 866 TATTGCGACGAGGGCTAAAGATTGGGAAGCGATGACGTTCCGTGGGAACAGACGCC 925
DB 221 TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
QY 926 AGATGGTTCGACCCGCTGCCGTACGTGCAATTGGTGAAGAGACGTGACTACATTCAAGAG 985
DB 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys 260
QY 986 GTGAAGTCGAGGCCACTGCGATATCTGCTAGCGGAAGAAACAGGCCGCCCAATGAT 1045
DB 261 ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGlnAlaAlaThrAsnAsp 280
QY 1046 TCGACTAAGAACGTCGCCCAAGAGGGCGGAGAAACATTTGATGACTCTAAATATGTAA 1105
DB 281 SerThrLysAsnValAlaGlnGluGlyGluLysHisLeuAspAspSerLysIleCysLys 300
QY 1106 ATATGTTATTCGAGAGCGGTAAACGTGTGCTTCGTCGCGCCACAGTGGCGCTGC 1165
DB 301 IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValAlaCys 320
QY 1166 GCCAAGTGGCGCGCTGTCGACGAGACAGTCCCGCATGTGTGCGACGAGCGTTCACGAATGCG 1225
DB 321 AlaLysCysAlaLeuSerThrAspLysCysPrometCysArgArgThrPheThrAsnAla 340
QY 1226 GTGCGGCTCTACTTCTCG 1243
DB 341 ValArgLeuTyrPheSer 346

RESULT 2

AAE07881
ID AAE07881 standard; protein; 377 AA.

XX AAE07881;

DT 01-NOV-2001 (first entry)

XX Fall armyworm inhibitor of apoptosis (IAP) protein.

XX Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW myocardial infarction; stroke; reperfusion injury; cancer; nootropic;
KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW neuroprotective; antianaemic; cardiant; cerebroprotective; vulnerary;
KW cyostatic; immunosuppressive; virucide; antialcoholic.

OS Spodoptera frugiperda.

XX WO200159108-A2.

PN 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US004071.

XX 10-FEB-2000; 2000US-00502528.

XX (REGC) UNIV CALIFORNIA.

PA (MAED/) MAEDA H.

XX Maeda S, Hammock BD, Huang Q, Maeda H;

PI WPI; 2001-514667/56.

XX N-PSDB; AAD14419.
PT Novel nucleic acid construct comprising cDNA encoding inhibitor of

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2005, 10:10:03 ; Search time 224 Seconds
(without alignments)
2503.116 Million cell updates/sec

Title: US-10-041-859A-1
Perfect score: 3773
Sequence: 1 cattattaactcacttcac.....tgcgcctcactctcgtga 3773

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91.8	2.4	1068	US-11-135-855-21	Sequence 21, Appl
2	81	2.1	769	US-11-135-855-22	Sequence 22, Appl
3	47.4	1.3	3159	US-10-793-626-4112	Sequence 4112, Ap
4	47.4	1.3	3376	US-10-793-626-4055	Sequence 4055, Ap
5	46.2	1.2	4248	US-10-793-626-3669	Sequence 3669, Ap
6	45.2	1.2	3073	US-10-793-626-3606	Sequence 3606, Ap
7	42.6	1.1	3549	US-10-793-626-4022	Sequence 4022, Ap
8	42.2	1.1	1314	US-11-074-176-151	Sequence 151, App
9	42.2	1.1	3478	US-10-793-626-3605	Sequence 3605, Ap
10	41	1.1	3165	US-10-793-626-3360	Sequence 3360, Ap
11	40.8	1.1	1299	US-10-793-626-779	Sequence 779, App
12	40.8	1.1	3119	US-10-793-626-4270	Sequence 4270, Ap
13	40.8	1.1	3393	US-10-793-626-4010	Sequence 4010, Ap
14	40.8	1.1	3645	US-10-793-626-4110	Sequence 4110, Ap
15	40.8	1.1	4017	US-10-793-626-4104	Sequence 4104, Ap
16	40.6	1.1	3458	US-10-793-626-3510	Sequence 3510, Ap
17	40.2	1.1	3189	US-10-793-626-3694	Sequence 3694, Ap
18	40.2	1.1	340000	US-11-102-978-3	Sequence 3, Appli
19	40	1.1	1644	US-11-077-550-23	Sequence 23, Appl
20	40	1.1	2097	US-10-793-626-2387	Sequence 2387, Ap
21	40	1.1	2574	US-11-077-550-21	Sequence 21, Appl
22	40	1.1	2574	US-11-077-550-27	Sequence 27, Appl
23	40	1.1	3028	US-10-793-626-4247	Sequence 4247, Ap

C	24	40	1.1	3337	1	US-10-793-626-3655	Sequence 3655, Ap
C	25	40	1.1	3350	1	US-10-793-626-4018	Sequence 4018, Ap
C	26	40	1.1	3509	9	US-11-077-550-19	Sequence 19, Appl
C	27	39.8	1.1	2902	1	US-10-793-626-4170	Sequence 4170, Ap
C	28	39.8	1.1	3617	1	US-10-131-826A-409	Sequence 409, App
C	29	39.4	1.0	3111	1	US-10-793-626-4268	Sequence 4268, Ap
C	30	39.4	1.0	3137	1	US-10-793-626-3575	Sequence 3575, Ap
C	31	39.4	1.0	3927	1	US-10-793-626-4223	Sequence 4223, Ap
C	32	39.4	1.0	3961	1	US-10-793-626-3597	Sequence 3597, Ap
C	33	39.4	1.0	4094	1	US-10-793-626-3641	Sequence 3641, Ap
C	34	39.4	1.0	4189	1	US-10-793-626-3898	Sequence 3898, Ap
C	35	39.4	1.0	4248	1	US-10-793-626-3669	Sequence 3669, Ap
C	36	39.2	1.0	3506	1	US-10-793-626-3423	Sequence 3423, Ap
C	37	39	1.0	2476	1	US-10-131-826A-489	Sequence 489, App
C	38	39	1.0	3462	1	US-10-793-626-4440	Sequence 4440, Ap
C	39	39	1.0	3536	1	US-10-793-626-4139	Sequence 4139, Ap
C	40	39	1.0	3939	1	US-10-793-626-3938	Sequence 3938, Ap
C	41	38.8	1.0	2683	1	US-10-793-626-3709	Sequence 3709, Ap
C	42	38.8	1.0	3008	1	US-10-793-626-3513	Sequence 3513, Ap
C	43	38.8	1.0	3037	1	US-10-793-626-3901	Sequence 3901, Ap
C	44	38.8	1.0	3073	1	US-10-793-626-3606	Sequence 3606, Ap
C	45	38.8	1.0	3116	1	US-10-793-626-4248	Sequence 4248, Ap

ALIGNMENTS

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RESULT 1
US-11-135-855-21
; Sequence 21, Application US/11135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-21

Query Match      2.4%; Score 91.8; DB 7; Length 1068;
Best Local Similarity 60.7%; Pred. No. 1.2e-10;
Matches 150; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 745 CACCGAGCGCGCGCTCGCCACCTTCAAGACTGCCGAGACGATATGCCCAAAACC 804
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QY 805 CCAAGAACTGGCAGAGCGCGGATTTCTTATACAGGCCAAGGTACAAAACGAATGCTT 864
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Db  315 CGAGCTGCTGCTGCTGCTGCGGCTTCTTCCACACAGGCCATCAGGACAAAGGTGAGTGCTT 374

QY 865 CTATTGCGACGAGCGGCTAAAGATTGGGAAAGCATGACGTTCCGTGGGAACGACGCC 924
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  375 CTCTGCTATAGGGGCGCTGCAGAGCTGGAAGCGCGGGAGCGACCCCTGAGCGAGCATGC 434

QY 925 CAGATGTTGACCGCTGCGCGCTACGTGCAATTGTTGAAAGAGCGTACTACATTCAGAA 984
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Db  435 CAAGTGTTCCCAAGCTGTCAATTCTGCTCCGGTCAAAAAGAAAGACTTTGTCCACAG 494
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OY 985 GGTGAAG 991
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Db 495 TGTGCAG 501

RESULT 2
US-11-135-855-22

; Sequence 22, Application US/11135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 22
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-22

Query Match 2.1%; Score 81; DB 7; Length 769;
Best Local Similarity 60.7%; Pred. No. 1.9e-08;
Matches 150; Conservative 0; Mismatches 95; Indels 2; Gaps 1;

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Db 255 CTCTGAGGAGTTGCGTCTGGCTCTTCTATGACTGGCCGCTGACTGTGAGTGCCACC 314
OY 805 CGAGGAAGTGGCAGAGCGCGGATTTCTTATACAGAGCCAAAGTGACAAACGAATGCTT 864
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Db 315 CGAGCTGCTGGCTGCTGCCGCTTCTTCCACACAGGCCCATCAGACAAAGGTGAGTGCTT 374
OY 865 CTATTGCGACGAGGGCTAAAGATTGGGAAAGCGATGACGTTCCGTGGGAACAGCACCC 924
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Db 375 CTTCCTATGAGGGGCTTGACAGCTGGAAGCGGGGACGACCCCTGGACGAGCATGC 434
OY 925 CAGATGTTGACCGCTGCGCGTACGTGCAATTGGTGAAGAGACGTGACTACATTCAAGAA 984
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Db 435 CAAGTGCTTC-CCCCGTGCAAGTTCTGCTCCGTCAAAGAAAGAGACTTTGTCCACAG 492
OY 985 GGTGAAG 991
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Db 493 TGTGCAG 499

RESULT 3
US-10-793-626-4112/c
; Sequence 4112, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4112

; LENGTH: 3159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4112

Query Match 1.3%; Score 47.4; DB 1; Length 3159;
Best Local Similarity 45.3%; Pred. No. 0.42;
Matches 216; Conservative 0; Mismatches 256; Indels 5; Gaps 1;

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Db 2271 TATTTAATFAGCATATCCATTCTTATTTTACAATCTTTATTTGCTTCTCTAATAT 2212
OY 1914 TACTATTATGATTAATTTCTGACATATTTATGSCAATTCGTAAGATACATCCAATA 1973
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Db 2211 CATTTTACATTAAGAACTTTATCATATTTAGAACAATTTTAACTGAATAAAATA 2152
OY 1974 CTTATTCATGTAATCTCACTTCAAAATGATGAATGTGTGTGATTAATGTTAAT 2033
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Db 2151 TGACTAAATCGTTTATCATTTTAAATATGATTCATCCTAGATATGTTTCTTTTAATTT 2092
OY 2034 GTCTAATTATTAATTAATTTGAGCAAGTTGCATTTAATGTATGATACTAATTATGTT 2093
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Db 2091 CTGTAAATTTTGAAGAAATTTGTAATATAGAAACATAT----TCTACACTATCTAGTT 2037
OY 2094 TTAACAAACATTTTAAGTATATATCTGCTGTGATTTTAATGTATCAAGAAATAACCCCA 2153
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Db 2036 TCAATTTTCCATTAATAATTAATGATTAATCGTGTTTAATATAACTAATAATATATGAA 1977
OY 2154 ACACCTTAATTGAAGTTTTCATATGTTGCTGTGATTAAGAAATCAATCAATTACATTTA 2213
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Db 1976 ACAAGCCAATGTAAAGTGCTTTTATTTTAAATAAAATATATTTCTTTATGATATTA 1917
OY 2214 CAAGTCAATTTTAATTTGTTCAGAAACCAACAATTTTGTAGTACTCCTGCTTACG 2273
|||
Db 1916 AAATTAATGAGGATTTGACGTTATGCTTAATTTATTTATTTATTTACTGGAACGCGTGG 1857
OY 2274 AAGTAGTATGACAAACCAAGTGTTCGTGATTTGCATTAATTTAGTTGAACCAATAT 2330
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Db 1856 ATTAATTAATTTACTCGCATATATACTGATGAATATTAATCATTTTAAACAATGAT 1800

RESULT 4
US-10-793-626-4055/c
; Sequence 4055, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4055
; LENGTH: 3376
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4055

Query Match 1.3%; Score 47.4; DB 1; Length 3376;
Best Local Similarity 44.9%; Pred. No. 0.43;
Matches 260; Conservative 0; Mismatches 316; Indels 3; Gaps 2;

OY 1770 ATTCTAATGTAATCCAGAGTTTAATATGTCGTCATTAATTAATATAAGAAACAAGTTTAC 1829

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Searched: 9793542 segs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	142.4	3.8	50000	8 US-10-706-635-23	Sequence 23, Appl
3	130.4	3.5	794	8 US-10-706-635-4	Sequence 4, Appli
4	111.8	3.0	8056	8 US-10-473-126-386	Sequence 386, App
5	109.8	2.9	8056	8 US-10-473-126-386	Sequence 386, App
6	104	2.8	1317	7 US-10-267-502-202	Sequence 202, App
7	104	2.8	1858	10 US-11-097-143-28832	Sequence 28832, A
8	104	2.8	2013	10 US-11-097-143-12365	Sequence 12365, A
9	104	2.8	10432	10 US-11-097-143-12364	Sequence 12364, A
10	104	2.8	14250	10 US-11-097-143-28831	Sequence 28831, A
11	99.8	2.6	3673778	6 US-10-312-841-2	Sequence 2, Appli
12	95.6	2.5	8056	8 US-10-473-126-240	Sequence 240, App
13	94.6	2.5	5979	5 US-10-239-676-18	Sequence 18, Appl
14	94.6	2.5	5979	6 US-10-240-453-26	Sequence 26, Appl
15	94.2	2.5	8056	8 US-10-473-126-240	Sequence 240, App
16	93.2	2.5	74665	8 US-10-719-993-6854	Sequence 6854, Ap
17	91.8	2.4	843	5 US-10-244-586-2	Sequence 2, Appli
18	91.8	2.4	1068	6 US-10-203-708-21	Sequence 21, Appl
19	91.8	2.4	1168	6 US-10-188-646-12	Sequence 12, Appl
20	91.8	2.4	1260	6 US-10-188-646-4	Sequence 4, Appli
21	91.8	2.4	1268	8 US-10-807-897-28	Sequence 28, Appl
22	91.8	2.4	1322	8 US-10-807-897-26	Sequence 26, Appl
23	91.8	2.4	1337	5 US-10-235-026-1	Sequence 1, Appli

24	91.8	2.4	1363	8 US-10-839-882-37	Sequence 37, Appl
25	91.8	2.4	1376	5 US-10-244-586-1	Sequence 1, Appli
26	88.2	2.3	5979	5 US-10-239-676-18	Sequence 18, Appl
27	88.2	2.3	5979	6 US-10-240-453-26	Sequence 26, Appl
28	88	2.3	399	9 US-10-983-495-1	Sequence 1, Appli
29	87.8	2.3	635	3 US-09-991-936-1622	Sequence 1622, Ap
30	87.8	2.3	635	9 US-10-978-245-1622	Sequence 1622, Ap
31	86.6	2.3	3673778	6 US-10-312-841-1	Sequence 1, Appli
32	85.2	2.3	3673778	6 US-10-312-841-1	Sequence 1, Appli
33	82	2.2	8310	8 US-10-861-875-9	Sequence 9, Appli
34	81	2.1	769	6 US-10-203-708-22	Sequence 22, Appl
35	78	2.1	614	9 US-10-450-763-27354	Sequence 27354, A
36	78	2.1	615	7 US-10-296-115-63	Sequence 63, Appl
37	77.8	2.1	14919	7 US-10-221-714A-228	Sequence 228, App
38	77.4	2.1	5611	7 US-10-433-793-100	Sequence 100, App
39	77	2.0	16217	6 US-10-311-455-597	Sequence 597, App
40	76.8	2.0	15548	6 US-10-311-455-2128	Sequence 2128, Ap
41	76.8	2.0	176096	9 US-10-981-277-34	Sequence 34, Appl
42	76.6	2.0	115218	8 US-10-278-698-255	Sequence 255, App
43	76.6	2.0	115218	8 US-10-278-698-769	Sequence 769, App
44	75.8	2.0	15373	6 US-10-311-455-439	Sequence 439, App
45	75.6	2.0	6013	7 US-10-221-613-226	Sequence 226, App

ALIGNMENTS

RESULT 1
US-10-041-859-1
; Sequence 1, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041,859
; PRIORITY FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3773
; TYPE: DNA
; ORGANISM: Bombyx mori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2733)..(3770)
US-10-041-859-1

Query Match 100.0%; Score 3773; DB 5; Length 3773;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	TTTAGTGTCTACTGCTTCTGTCTGGCTGCGTTGACGTTTGGAACTTCACTATTGTTG	120
DB	61	TTTAGTGTCTACTGCTTCTGTCTGGCTGCGTTGACGTTTGGAACTTCACTATTGTTG	120
QY	121	TTCTGCAAGACGAGTGTCAGTGATTAAACAAAACATAAGATAGACGTTTATGCGTT	180
DB	121	TTCTGCAAGACGAGTGTCAGTGATTAAACAAAACATAAGATAGACGTTTATGCGTT	180
QY	181	ACTAAAAAAGAAAAATATACCAATGAGTTCGAAAGTTGCTAAAAATGAGAGCTGC	240
DB	181	ACTAAAAAAGAAAAATATACCAATGAGTTCGAAAGTTGCTAAAAATGAGAGCTGC	240

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Db 301 GCTCATGTTATCCTCGTGGAGTCTTCAACGACATCCACACTCCCGTCACTTCGTGTC 360
QY 361 AGCTGATAAAAACGATAAATCAGACACATTTCAACTTCCTCTGATATGCGCGACATGCG 420
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Db 421 TCGTGAAGAGAACGCTTGAAAAACATTTGATCAGTGGCCCGTTACGTTTGTGACCGCGGA 480
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QY 661 GACCGCTGTGCTAGAGACGAATGTGGGGCCAGTGCGCCACGACGCTCCCGCATGCC 720
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Db 1141 GCCGTGCGSCACGTGGTGGCTGCGCCCAAGTGGCGCTGTGACGAGCAAGTGGCCGAT 1200
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| | | | |
Db 1201 GTGTGCGAGACGTTCAAGATGCGGTGCGGCTCTACTTCTGCTGAAGGACCTCTCG 1260
QY 1261 CGAGCTGTATATCAATCACTTCAACCGGGCGGCTCTGAGCGGTGCTGAAACCACTTTCGA 1320
| | | | |
Db 1261 CGAGCTGTATATCAATCACTTCAACCGGGCGGCTCTGAGCGGTGCTGAAACCACTTTCGA 1320

QY 1321 ACGAAACCGCGTATCCGTGTGATTTTACATTAATAATTACAAATTGATAGCGGTGG 1380
| | | | |
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QY 1381 GCAATGTATAGGAACCTCGTCAGAACTCCCGAGTTGACGTGCAGGAAGGAGTTAGTATTT 1440
| | | | |
Db 1381 GCAATGTATAGGAACCTCGTCAGAACTCCCGAGTTGACGTGCAGGAAGGAGTTAGTATTT 1440
QY 1441 GTAACCTGTAAACGTATGTTGAATGATTTTATTATTAAATTTCTAATGACAAA 1500
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Db 1441 GTAACCTGTAAACGTATGTTGAATGATTTTATTATTAAATTTCTAATGACAAA 1500
QY 1501 GTGTAAGTAAATAAATGTACATATTATTGATTTATCAGTTTGTCCGACCAAAAAGT 1560
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Db 1501 GTGTAAGTAAATAAATGTACATATTATTGATTTATCAGTTTGTCCGACCAAAAAGT 1560
QY 1561 GAAATGTACATAGGTTTTTCATATCACTTCAACAGTCCGAGACCTTCTTTTGAATTTA 1620
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Db 1561 GAAATGTACATAGGTTTTTCATATCACTTCAACAGTCCGAGACCTTCTTTTGAATTTA 1620
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QY 1921 TATTGATTAATTTCTGACATTAATTTATGGCAATTCGCTAAGATACAATCCAATCTTATTT 1980
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QY 2221 ATTTTAATTGTTCAGAAACCAAAACACAATTTTGTAGTACTCCGTGTTACGAAGTAGT 2280
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Db 2221 ATTTTAATTGTTCAGAAACCAAAACACAATTTTGTAGTACTCCGTGTTACGAAGTAGT 2280
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Db 2341 CATTTTAAGATGTCATTGAAGGAATTCGTATTAATAAATGGGAATTTATTTGCTGTAT 2400
QY 2401 AATACAATCCCGCAACAAGCAATTTGCAAGTTTCTACACAATAAACGATATTGTATCCAT 2460
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Run on: November 26, 2005, 00:34:47 ; Search time 624 Seconds
(without alignments)
10747.981 Million cell updates/sec

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Perfect score: 3773
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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	437.2	11.6	1134	3	US-09-502-528-2 Sequence 2, Appli
3	142.4	3.8	50000	3	US-09-662-254B-23 Sequence 23, Appl
4	130.4	3.5	794	3	US-09-662-254B-4 Sequence 4, Appli
5	104	2.8	1304	3	US-09-586-305A-8 Sequence 8, Appli
6	104	2.8	1317	3	US-09-586-305A-1 Sequence 1, Appli
7	104	2.8	1317	3	US-09-586-305A-2 Sequence 2, Appli
8	104	2.8	1317	3	US-09-586-305A-3 Sequence 3, Appli
9	104	2.8	1317	3	US-09-586-305A-5 Sequence 5, Appli
10	104	2.8	1317	3	US-09-586-305A-6 Sequence 6, Appli
11	104	2.8	1317	3	US-09-586-305A-7 Sequence 7, Appli
12	104	2.8	1317	3	US-09-586-305A-9 Sequence 9, Appli
13	104	2.8	1317	3	US-09-586-305A-10 Sequence 10, Appl
14	102.4	2.7	1317	3	US-09-586-305A-4 Sequence 4, Appli
15	97.4	2.6	18773	3	US-09-949-016-14164 Sequence 14164, A
16	91.8	2.4	1260	3	US-09-949-016-1949 Sequence 1949, Ap
17	91.8	2.4	1337	3	US-09-127-928-1 Sequence 1, Appli
18	81.4	2.2	18773	3	US-09-949-016-14164 Sequence 14164, A
19	79.8	2.1	187169	3	US-09-949-016-12776 Sequence 12776, A
20	79.8	2.1	191569	3	US-09-949-016-15940 Sequence 15940, A
21	78	2.1	1141	3	US-09-806-708B-22 Sequence 22, Appl
22	76.4	2.0	95255	3	US-09-949-016-17067 Sequence 17067, A
23	75.2	2.0	205044	3	US-09-949-016-15851 Sequence 15851, A
24	75.2	2.0	205044	3	US-09-949-016-15852 Sequence 15852, A

C	25	75.2	2.0	205044	3	US-09-949-016-15853	Sequence 15853, A
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	30	74	2.0	1448	3	US-09-579-692B-57	Sequence 57, Appl
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	34	74	2.0	2601	3	US-09-689-366-3	Sequence 3, Appli
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	36	74	2.0	2601	6	PCT-US96-12860-3	Sequence 3, Appli
	37	74	2.0	2676	2	US-08-511-485-5	Sequence 5, Appli
	38	74	2.0	2676	3	US-09-201-936-5	Sequence 5, Appli
	39	74	2.0	2676	3	US-09-011-356-5	Sequence 5, Appli
	40	74	2.0	2676	3	US-09-672-717-220	Sequence 220, App
	41	74	2.0	2676	3	US-09-201-932-5	Sequence 5, Appli
	42	74	2.0	2916	3	US-09-814-915A-31	Sequence 31, Appli
	43	74	2.0	3076	2	US-09-205-144-1	Sequence 1, Appli
	44	74	2.0	3076	3	US-09-814-915A-11	Sequence 11, Appl
	45	74	2.0	3165	3	US-09-949-016-160	Sequence 160, App

ALIGNMENTS

RESULT 1
US-09-502-528-1
; Sequence 1, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502, 528
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfiAP) nucleotide sequence including 5' and 3'
; OTHER INFORMATION: untranslated regions, full length SfiAP cDNA
; NAME/KEY: CDS
; LOCATION: (229)..(1362)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfiAP)
US-09-502-528-1

Query Match 11.7%; Score 441.8; DB 3; Length 1739;
Best Local Similarity 69.7%; Pred. No. 2.5e-94;
Matches 650; Conservative 0; Mismatches 262; Indels 21; Gaps 3;

QY	343	CCCCGACCTTCGTCGTCAGCTGATAAACGGATAATGACACACATTCACCTCTCC	402
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QY	403	TGATATGCCGACATGCGTCGTGAAGAGAAAGCTGAAACATTGATCAGTGGCCCGT	462
DB	504	GGACACAGTGTGATATGAAAGAGATGAACGTATGAAACATTGAAAAATGCCCCGT	563
QY	463	TACGTTTGTGACCGCCGAAACAATTGGCCCGCAACGATTTACTACCTCGTCCGCCGA	522
DB	564	AAATTTCATATCCGAGAGCAACTGCTCGAAATGATTTTACTACCTCGGCCGTAGAGA	623
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Db 684 TCGGAAGGACCATCAGCGTTGGGGCGCCACAGTCCCATTTTGTGCGCA--AAATTGAACGG 740
QY 643 CAACGCTGGGGAGAGGGGACCCGCTGTCCGCTAGAGCAATGTGGGGCCAGTGGGC-- 699
Db 741 TACTGCAGCAGACAGCGGGTAGTTCGGGCCAGAGCAGTGTGTGCCCCGCGCTCC 800
QY 700 -----CAGCAGCCCTCCCGCCATGCCCCCGCCCGCCGCGGCTACTCCACGAGGC 753
Db 801 CTCGGTACCTCTCCCGCGGTATGGCCGGTCCCGTGCACCCAGATATGCATCTGAAGC 860
QY 754 CGCGCGCTCGCCACTTCAAGACTGGCCGAGACGTATGCGCAAAAACCAGGAACT 813
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QY 814 GGCAGAGCCCGATTCTCTATACAGGCCCAAGTGACAAACGAATGCTTCTATTGCGA 873
Db 921 CGCCGAGGCTGCTTTTAACTGTGTCAGGGAGACAAAACCAAGTGTTTATTGCGA 980
QY 874 CGGAGGGCTAAAAGATTGGGAAAAGCGATGACGTTCCGTGGGAAACAGACGCCAGATGTT 933
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Db 1341 AGTGGGTTATATTCTCGTGAAGAGCCACC 1373

RESULT 2
US-09-502-528-2
; Sequence 2, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: Sf1AP nucleotide sequence, open reading frame
; OTHER INFORMATION: (ORF) only

; NAME/KEY: CDS
; LOCATION: (1)..(1134)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (Sf1AP)
US-09-502-528-2
Query Match 11.6%; Score 437.2; DB 3; Length 1134;
Best Local Similarity 69.7%; Pred. No. 2.6e-93;
Matches 643; Conservative 0; Mismatches 258; Indels 21; Gaps 3;
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QY 403 TGATATGCCGACATGCGTGTGAAGAGAACGTTGAAAACATTGATCAGTGGCCCGT 462
Db 276 GGACACAGTTGATATGAGAAAAAGAGATGAACGTATGAAAACATTGAAAATGGCCCGT 335
QY 463 TACGTTTTGACGCCGGAACAATTGGCCCGCAAGATTCTACTACCTCGGTGCGCGA 522
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QY 1225 GGTGCGGCTTACTTCTCGTGA 1246
Db 1113 AGTGGGTTATATTCTCGTGA 1134

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

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Maximum Match 100%
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11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	639.8	17.0	658	7	CK505037 rswcc0_00
6	598.6	15.9	626	8	DN237202 EST00327
7	588.4	15.6	612	7	CK518109 rswjbd_00
8	577	15.3	624	7	CK564268 rswpbd_00
9	575.8	15.3	666	8	DN237481 EST00607
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11	546.6	14.5	633	7	CK495885 rswpbd_00
12	521.4	13.8	622	7	CK497882 rswpbd_00
13	518.6	13.7	585	8	DN237482 EST00608
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29	114	3.0	712	3	BM601939	BM601939 170006870
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33	108.8	2.9	727	6	CF525095	CF525095 AGENCOURT
34	108.8	2.9	788	8	DN069067	DN069067 JGI CABD5
35	105.6	2.8	547	10	AG973047	AG973047 Drosophila
36	105.6	2.8	592	2	BE978623	BE978623 bs80h08.y
37	105.6	2.8	878	8	CA981117	CX498117 JGI XZG43
38	105.2	2.8	937	6	CA981608	CA981608 AGENCOURT
39	104.4	2.8	1489	10	AG350139	AG350139 Mus muscu
40	104	2.8	678	6	CA805412	CA805412 EGG0118a.
41	102.8	2.7	1261	8	DN682799	DN682799 CGX26-C05
42	102.4	2.7	1101	10	CNS00EVL	AL069706 Drosophila
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ALIGNMENTS

RESULT 1
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LOCUS BP121000 cen- Bombyx mori cDNA clone cen-4016, mRNA sequence.
DEFINITION BP121000
ACCESSION BP121000
VERSION BP121000.1 GI:29554042

KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori

REFERENCE
AUTHORS Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
TITLE Bombyx mori cDNA (Mita,K. 2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Mita K

Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6121
Email: kmita@nias.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3').

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/tissue_type="compound eye"
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/note="mixed stages from 5th instar larva to pupa"

ORIGIN
Query Match 18.7%; Score 705.6; DB 3; Length 712;
Best Local Similarity 99.4%; Pred. No. 1.2e-132;
Matches 708; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 665 GCTGTGGTAGAGACGAATGTGGGGCCAGTGGCGGCACGACGCTCCCGCATGCCCCGCG 724
Db 1 GCTGTGGTAGAGACGAATGTGGGGCCAGTGGCGGCACGACGCTCCCGCATGCCCCGCG 60
Qy 725 CCCGTGACGCGCGGTACTCCACCGAGGCCGCGCGGCTGCCACCTTCAAGGACTGGCCG 784

|||||
Db 61 CCGGTGCACGCGCGGTACTTCACCGAGGCCGCGCGGTGCGCACCTTCAAGGACTGCGCG 120
QY 785 AGACGTATGCGCCAAAACCCGAGGAACCTGGCAGAGCCGGATTCTTCTATACAGGCCAA 844
Db 121 AGATGTATGCGCCAAAACCCGAGGAACCTGGCAGAGCCGGATTCTTCTATACAGGCCAA 180
QY 845 GGTGACAAAACGAAATGCTTCTATTGCGACGAGGCGTAAAGATTGGAAAAGCGATGAC 904
Db 181 GGTGACAAAACGAAATGCTTCTATTGCGACGAGGCGTAAAGATTGGAAAAGCGATGAC 240
QY 905 GTTCCGTGGAAACAGCAGCCGAGATGGTTCGACCCGCTGCCGTACGTGCAATTGTGAAA 964
Db 241 GTTCCGTGGAAACAGCAGCCGAGATGGTTCGACCCGCTGCCGTACGTGCAATTGTGAAA 300
QY 965 GGAAGTACTACATTCAAGAGGTGAAGTGGAGGCCACTGCGATATCTGCTAGCGAAGAA 1024
Db 301 GGAAGTACTACATTCAAGAGGTGAAGTGGAGGCCACTGCGATATCTGCTAGCGAAGAA 360
QY 1025 GAACAGGCCCGCCCAATGATTGCACTAAGAACGTGCCCAAGAGGGCGAGAAACATTG 1084
Db 361 GAACAGGCCCGCCCAATGATTGCACTAAGAACGTGCCCAAGAGGGCGAGAAACATTG 420
QY 1085 GATGACTCTAAAATATGTAAATATGTTATTCCGAGAGCGTAAAGTGTGCTTGTGCGCG 1144
Db 421 GATGACTCTAAAATATGTAAATATGTTATTCCGAGAGCGTAAAGTGTGCTTGTGCGCG 480
QY 1145 TGGCGCCACAGTGTGCGCGTGCAGCAAGTGCAGCGCGCTGTGCAAGCAAGTGCAGTGT 1204
Db 481 TGGCGCCACAGTGTGCGCGTGCAGCAAGTGCAGCGCGCTGTGCAAGCAAGTGCAGTGT 540
QY 1205 CGCAGGACGTTCAAGATGCGCGTGCAGTCTTCTGCTGAAAAGAACCCCTCTGCGAG 1264
Db 541 CGCAGGACGTTCAAGATGCGCGTGCAGTCTTCTGCTGAAAAGAACCCCTCTGCGAG 600
QY 1265 CTGTATACTAATCACTTCAACGGGCGCGCTGAGCGGTGTAAGAACCAACCTTCGAACGA 1324
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QY 1325 AACCGCGTATCCTGTGATTTTACATTAAATTAATTAACAATTGATAGCGG 1376
Db 661 AACCGCGTATCCTGTGATTTTACATTAAATTAATTAACAATTGATAGCGG 712

RESULT 2
BP120885 727 bp mRNA linear EST 16-MAY-2003
LOCUS BP120885 cen- Bombyx mori cDNA clone cen-3830, mRNA sequence.
DEFINITION BP120885
ACCESSION BP120885
VERSION BP120885.1 GI:29553920
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
REFERENCE 1 (bases 1 to 727)
AUTHORS Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
TITLE Bombyx mori cDNA (Mita,K. 2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6121
Email: kmitsa@nias.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3').

FEATURES
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/organism="Bombyx mori"
/mol_type="mRNA"

/db_xref="taxon:7091"
/clone="cen-3830"
/issue_type="compound eye"
/clone_id="cen-"
/note="mixed stages from 5th instar larva to pupa"

Query Match 18.2%; Score 685.6; DB 3; Length 727;
Best Local Similarity 99.0%; Pred. No. 1.3e-128;
Matches 721; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

QY 665 GCTGTCCGTAGAGACGAATGTGGGGCCAGTGCAGCCACGACGCTCCCCGATGCCCGC 724
Db 1 GCTGTCCGTAGAGACGAATGTGGGGCCAGTGCAGCCACGACGCTCCCCGATGCCCGC 60
QY 725 CCCGTGCACGCGCGTACTCCACCAGAGGCCGCGCGCTCGCCACCTTCAAGACTGGCGG 784
Db 61 CCCGTGCACGCGCGTACTCCACCAGAGGCCGCGCGCTCGCCACCTTCAAGACTGGCGG 120
QY 785 AGACGTATGCGCCAAAACCCGAGGAACCTGGCAGAGCCGGATTCTTCTATACAGGCCAA 844
Db 121 AGATGTATGCGCCAAAACCCGAGGAACCTGGCAGAGCCGGATTCTTCTATACAGGCCAA 180
QY 845 GGTGACAAAACGAAATGCTTCTATTGCGACGAGGGCTAAAGATTGGAAAAGCGATGAC 904
Db 181 GGTGACAAAACGAAATGCTTCTATTGCGACGAGGGCTAAAGATTGGAAAAGCGATGAC 240
QY 905 GTTCCGTGGAAACAGCAGCCCAAGATGTTTCAACCCGCTGCCGTACGTGCAATTGTGAAA 964
Db 241 GTTCCGTGGAAACAGCAGCCCAAGATGTTTCAACCCGCTGCCGTACGTGCAATTGTGAAA 300
QY 965 GGAAGTACTACATTCAAGAGGTGAAGTGGAGGCCCACTGCGATATCTGCTAGCGAAGAA 1024
Db 301 GGAAGTACTACATTCAAGAGGTGAAGTGGAGGCCCACTGCGATATCTGCTAGCGAAGAA 360
QY 1025 GAACAGGCCCGCCCAATGATTGCACTAAGAACGTGCCCAAGAGGGCGAGAAACATTG 1084
Db 361 GAACAGGCCCGCCCAATGATTGCACTAAGAACGTGCCCAAGAGGGCGAGAAACATTG 420
QY 1085 GATGACTCTAAAATATGTAAATATGTTATTCCGAGAGCGTAAAGTGTGCTTGTGCGCG 1144
Db 421 GATGACTCTAAAATATGTAAATATGTTATTCCGAGAGCGTAAAGTGTGCTTGTGCGCG 480
QY 1145 TGGCGCCACAGTGTGCGCGTGCAGCAAGTGCAGCGCGCTGTGCAAGCAAGTGCAGTGT 1204
Db 481 TGGCGCCACAGTGTGCGCGTGCAGCAAGTGCAGCGCGCTGTGCAAGCAAGTGCAGTGT 540
QY 1205 CGCAGGACGTTCAAGATGCGCGTGCAGTCTTCTGCTGAAAAGAACCCCTCTGCGAG 1264
Db 541 CGCAGGACGTTCAAGATGCGCGTGCAGTCTTCTGCTGAAAAGAACCCCTCTGCGAG 600
QY 1265 CTGTATACTAATCACTTCAACGGGCGCGCTGAGCGGTGTAAGAACCAACCTTCGAAC 1322
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QY 1323 GAAACCGCGTATCCTGTGATTTTACATTAAATTAATTAACAATTGATAGCGGTGGGC 1382
Db 661 GAAACCGCGTATCCTGTGATTTTACATTAAATTAATTAACAATTGATAGCGGTGGGC 719
QY 1383 AATGTATA 1390
Db 720 AATGTATA 727

RESULT 3
AV401669 723 bp mRNA linear EST 01-MAR-2005
LOCUS AV401669 Bombyx mori C108 spinning stage day-0 Bombyx mori cDNA
DEFINITION AV401669 clone hes00025 T3, mRNA sequence.
ACCESSION AV401669
VERSION AV401669.1 GI:6905321
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2005, 22:06:22 ; Search time 2086 Seconds
(without alignments)
12054.595 Million cell updates/sec

Title: US-10-041-859A-1
Perfect score: 3773
Sequence: 1 cattactaacctcacttcac.....tgcgcctcactctctgtga 3773

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3773	100.0	3773	6	ABQ78228	Abq78228 Nucleotid
2	441.8	11.7	1739	5	AAD14419	Aad14419 Fall army
3	142.4	3.8	50000	6	ABL55643	Ab155643 AmEPV gen
4	130.4	3.5	794	6	ABI55635	Ab155635 AmEPV bac
5	111.8	3.0	8056	8	ABZ10246	Abz10246 Haematopo
6	109.8	2.9	8056	8	ABZ10246	Abz10246 Haematopo
7	105.6	2.8	1304	5	AAc84527	Aac84527 Drosophil
8	105.6	2.8	1317	5	AAc84520	Aac84520 Drosophil
9	105.6	2.8	1317	5	AAc84529	Aac84529 Drosophil
10	105.6	2.8	1317	5	AAc84521	Aac84521 Drosophil
11	105.6	2.8	1317	5	AAc84525	Aac84525 Drosophil
12	105.6	2.8	1317	5	AAc84522	Aac84522 Drosophil
13	105.6	2.8	1317	5	AAc84526	Aac84526 Drosophil
14	105.6	2.8	1317	5	AAc84528	Aac84528 Drosophil
15	105.6	2.8	1317	5	AAc84524	Aac84524 Drosophil
16	104	2.8	1317	5	AAc84523	Aac84523 Drosophil
17	104	2.8	1317	12	ADO07876	Ado07876 Fly polym
18	104	2.8	1858	4	ABL21061	Ab121061 Drosophil
19	104	2.8	2013	4	ABL10083	Ab110083 Drosophil

20	104	2.8	10432	4	ABL10082	Ab110082 Drosophil
21	104	2.8	14250	4	ABL21060	Ab121060 Drosophil
22	101	2.7	2131	14	ADZ71009	Adz71009 Human chr
23	96.4	2.6	110000	13	ABD32968_6	Continuation (7 of
24	95.6	2.5	8056	8	ABZ10100	Abz10100 Haematopo
25	94.6	2.5	5979	4	AAS45313	Aas45313 Chemical
26	94.6	2.5	5979	6	ABK28152	Abk28152 DNA trans
27	94.2	2.5	8056	8	ABZ10100	Abz10100 Haematopo
28	91.8	2.4	672	6	AAL42857	Aal42857 Survivin-
29	91.8	2.4	723	6	AAL42856	Aal42856 Survivin-
30	91.8	2.4	840	6	AAL42858	Aal42858 Survivin-
31	91.8	2.4	843	4	AAF24857	Aaf24857 Nucleotid
32	91.8	2.4	1068	4	AAD16364	Aad16364 Human SBh
33	91.8	2.4	1168	12	ADH89543	Adh89543 Human Liv
34	91.8	2.4	1260	12	ADH89535	Adh89535 Human Liv
35	91.8	2.4	1260	14	AEA36171	Aea36171 Human nuc
36	91.8	2.4	1268	10	ACC72844	Acc72844 Human can
37	91.8	2.4	1268	13	ADS71346	Ads71346 Human liv
38	91.8	2.4	1322	10	ACC72843	Acc72843 Human can
39	91.8	2.4	1322	13	ADS71344	Ads71344 Human liv
40	91.8	2.4	1337	3	AAZ61210	Aaz61210 DNA encod
41	91.8	2.4	1363	3	AAI5007	Aai5007 cDNA enco
42	91.8	2.4	1363	13	ADT88075	Adt88075 Human pro
43	91.8	2.4	1376	4	AAF24856	Aaf24856 Nucleotid
44	91.4	2.4	2482	14	ADZ71091	Adz71091 Human chr
45	90.6	2.4	1452	14	ADZ71095	Adz71095 Human chr

ALIGNMENTS

RESULT 1	
ABQ78228	ABQ78228 standard; cDNA; 3773 BP.
ID	ABQ78228;
AC	ABQ78228;
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	Nucleotide sequence of inhibitor of apoptosis protein BmiAP.
XX	
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;
KW	Spodoptera frugiperda; insult-resistant plant; caspase; gene; ss.
XX	
OS	Bombyx mori.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	2733. .3773
FT	/*tag= a
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PN	WO200253586-A2.
XX	
PD	11-JUL-2002.
XX	
PF	07-JAN-2002; 2002WO-US000314.
XX	
PR	08-JAN-2001; 2001US-0260478P.
XX	
PA	(BURN-) BURNHAM INST.
XX	
PI	Maeda S, Huang Q, Reed JC, Deveraux QL;
XX	
DR	WPI; 2002-590628/63.
DR	P-PSDB; ABB78046.
XX	
PT	Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT	member BmiAP from silkworm Bombyx mori BmiN cells, useful for inhibiting
PT	apoptosis and identifying an agent that modulates activity of
PT	polypeptide.
XX	
PS	Claim 8; Page 29-30; 62pp; English.
XX	

CC The present scone encodes a polypeptide which is an inhibitor of
CC apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is
CC derived from silkworm Bombyx mori Bm1AP polypeptide
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC mori cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insulnt-resistant plant. BmiAP is also
CC useful for inhibiting caspases

XX Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;

Query Match 100.0%; Score 3773; DB 6; Length 3773;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CATTATTAACCTCACTTCCTTCGGTAGTGTGAATGTTAACGTGAACCTCCGGCTCTTC 60
QY 61 TTTAGTTGCTACTCGGTTCTGTCTGGCTCGGTTGACGTTTGGAACTTCATACTATTG 120
Db 61 TTTAGTTGCTACTCGGTTCTGTCTGGCTCGGTTGACGTTTGGAACTTCATACTATTG 120
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Db 301 GCTCATGTTATCCTCGTGTGAGTCTTCAACGACATCCACACTCCCGTCACCTTCGTCTC 360
QY 361 AGCTGATAAAAACGATATCAACGACACATTCCTTCCTGATATGCGCGACATGCG 420
Db 361 AGCTGATAAAAACGATATCAACGACACATTCCTTCCTGATATGCGCGACATGCG 420
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QY 1741 GATTTCACTTCCCGTGTGAAGTGAATAAATCTAATGTAATCCAGAGTTTAAATGTCG 1800
Db 1741 GATTTCACTTCCCGTGTGAAGTGAATAAATCTAATGTAATCCAGAGTTTAAATGTCG 1800
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Db 1801 TCATTAATTAATTAAGAAACAAGTTTACGCTCTTTTGCTTGAAAAATCTTATAATTGA 1860
QY 1861 TTCAGGAATTATTAAATGTGACTATATTGTTCTGTAAATAACATTAATATACTATT 1920
Db 1861 TTCAGGAATTATTAAATGTGACTATATTGTTCTGTAAATAACATTAATATACTATT 1920
QY 1921 TATTGATTAATTGACATTAATTTATGGCAATTCCGTAAGATACAATCAATACTTATTT 1980

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 26, 2005, 20:56:58 ; Search time 131 Seconds
(without alignments)
392.507 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3205263 seqs, 74304013 residues

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360	19.1	769	7	US-11-135-855-22 Sequence 22, Appl
2	326	17.3	1068	7	US-11-135-855-21 Sequence 21, Appl
3	98.5	5.2	1725	1	US-10-821-234-772 Sequence 772, Appl
4	88.5	4.7	5682	7	US-11-059-982-2 Sequence 2, Appl1
5	86.5	4.6	1167	1	US-10-858-730-169 Sequence 169, App
6	85	4.5	2238	1	US-10-858-730-262 Sequence 262, App
7	84.5	4.5	2240	7	US-11-064-769-18 Sequence 18, Appl
8	84	4.5	1971	1	US-10-131-826A-225 Sequence 225, Appl

C	10	83	4.4	1899	1	US-10-689-742-77	Sequence 77, Appl
C	11	82	4.3	1611	1	US-10-980-388-2	Sequence 2, Appl1
C	12	82	4.3	1612	1	US-10-980-388-51	Sequence 51, Appl
C	13	81.5	4.3	1719	1	US-10-821-234-805	Sequence 805, App
C	14	81	4.3	3515	1	US-10-821-234-438	Sequence 438, App
C	15	79.5	4.2	1740	1	US-10-821-234-65	Sequence 65, Appl
C	16	79.5	4.2	3378	1	US-10-689-742-53	Sequence 53, Appl
C	17	79	4.2	1659	7	US-10-821-234-592	Sequence 592, App
C	18	78.5	4.2	3109	1	US-11-135-855-11	Sequence 11, Appl
C	19	78.5	4.2	5253	9	US-10-821-234-63	Sequence 63, Appl
C	20	78.5	4.2	8910	1	US-11-004-057-3	Sequence 3, Appl1
C	21	77.5	4.1	2736	1	US-10-821-234-281	Sequence 281, App
C	22	77	4.1	1482	9	US-10-821-234-55	Sequence 55, Appl
C	23	77	4.1	1932	7	US-11-082-389-197	Sequence 197, App
C	24	77	4.1	1956	1	US-11-137-465-21	Sequence 21, Appl
C	25	77	4.1	11337	1	US-10-499-715-1	Sequence 628, App
C	26	76	4.0	3734	1	US-10-131-826A-147	Sequence 147, App
C	27	76	4.0	5468	1	US-10-821-234-49	Sequence 49, Appl
C	28	76	4.0	43948	1	US-10-949-720-393	Sequence 393, App
C	29	75.5	4.0	987	1	US-10-821-234-819	Sequence 819, App
C	30	75	4.0	1731	7	US-10-821-234-819	Sequence 183, App
C	31	75	4.0	3721	1	US-11-074-176-183	Sequence 183, App
C	32	75	4.0	3911	9	US-10-131-826A-543	Sequence 543, App
C	33	75	4.0	4351	1	US-11-004-057-5	Sequence 5, Appli
C	34	74.5	3.9	1284	7	US-10-821-234-295	Sequence 295, App
C	35	74.5	3.9	1399	7	US-11-074-176-363	Sequence 363, App
C	36	74.5	3.9	1853	1	US-11-182-592-5	Sequence 5, Appli
C	37	74.5	3.9	2058	7	US-10-967-527A-1	Sequence 1, Appli
C	38	74.5	3.9	2388	1	US-11-065-943-57	Sequence 57, Appl
C	39	74	3.9	2112	1	US-10-821-234-252	Sequence 252, App
C	40	74	3.9	2754	1	US-10-821-234-465	Sequence 465, App
C	41	73.5	3.9	2737	1	US-10-821-234-163	Sequence 163, App
C	42	73	3.9	1854	9	US-10-131-826A-55	Sequence 55, Appl
C	43	72.5	3.8	4338	1	US-11-082-389-133	Sequence 133, App
C	44	72	3.8	1503	1	US-10-526-731-2	Sequence 2, Appli
C	45	72	3.8	1546	8	US-10-131-826A-363	Sequence 363, App
						US-11-112-944-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-11-135-855-22
: Sequence 22, Application US/1135855
: Publication No. US20050255557A1
: GENERAL INFORMATION:
: APPLICANT: SMITHKLINE BEECHAM CORPORATION
: APPLICANT: SMITHKLINE BEECHAM P.L.C.
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP50013
: CURRENT APPLICATION NUMBER: US/11/135, 855
: CURRENT FILING DATE: 2005-05-24
: PRIOR APPLICATION NUMBER: US/10/203, 708
: PRIOR FILING DATE: 2002-08-13
: PRIOR APPLICATION NUMBER: PCT/US01/04703
: PRIOR FILING DATE: 2001-02-14
: PRIOR APPLICATION NUMBER: 60/182,172
: PRIOR FILING DATE: 2000-02-14
: PRIOR APPLICATION NUMBER: 60/186, 084
: PRIOR FILING DATE: 2000-02-29
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 22
: LENGTH: 769
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-11-135-855-22

Alignment Scores:
Pred. No.: 5.74e-27 Length: 769
Score: 360.00 Matches: 91
Percent Similarity: 47.78% Conservative: 38
Best Local Similarity: 33.70% Mismatches: 103

Query Match: 19.08% Indels: 40
DB: 7 Gaps: 9

US-10-041-859A-2 (1-346) x US-11-135-855-22 (1-769)

QY 102 LeuGlyArgGlyAspGluValCysCysAlaPheCysIleValGluIleMetArgTrpVal 121
DB 1 ATGGGACCTAAAGACAGTGCCTGAGTGCCTGACCGTGAACACAGCCGAGCCACTGGGCA 60
QY 122 GluGlyAspAspProAlaAlaAspHisArgArgTrpAlaPro-----GlnCys 137
DB 61 GCCGGTGATGTCCTCCACGAGAG--CGCTG-TGGACCCCGCTCTGTGGGCAGCCCTGT 116
QY 138 Pro-----PheValArgLysGlnMetTyrAlaAsnAlaGlyGlu 151
DB 117 CCTAGGCTTGACACCTGACAGACCTGGAGCCAGTGAGTGGCAGATCCTGGGCAAGCT 176
QY 152 AlaThr-----AlaValGlyArg-AspGluCysGlyAlaSerAlaAlaThrGlnProPr 169
DB 177 GCGGCCCCGTACAGAGAGAGAGAGAGAGGCGCGGGGCCACCTGTGTCCAGGGGCC 236
QY 169 oArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPh 189
DB 237 TGCCTTCCCCGGC-----ATGGGCTGTAGAGAGTTGCGTGTGCTCCTCT 281
QY 189 eLysAspTrpProArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGlyPhePh 209
DB 282 CTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTGCTGGCTGCTCCGCTTCTT 341
QY 209 eTyrThrGlyGlnGlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLysAspTr 229
DB 342 CCACACAGGCCATCAGACAGAGTGAGTGCTTCTTCTATGAGGGCCGTGCAGAGCTG 401
QY 229 pGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAlaTyrVa 249
DB 402 GAAGCGCGGAGCAGCCCTGGACGAGCATGCAAGTGTTCCTTCCCTTCCCTTCCCT 459
QY 249 LglLeuValLysGlyArgAspTyrIleGlnLysValLysSerGluAlaThrAlaIleSe 269
DB 460 GCTCCGGTCAAAAGAGAGAGACTTGTCCACAGTGTGACAGAGACTCACTCCAGCTGCT 519
QY 269 rAlaSer-----GluGluGluGlnAlaAlaThrAsnAspSerThrLysAs 284
DB 520 GGGCTCCTGGGAGCCCGTGGGAAGAACCGGAAGACCGCAGCCCT----- 562
QY 284 nValAlaGlnGluGlyGlu-----LysHisLeuAspSerLy 297
DB 563 -GTGCCCCCTCCGAGCCAGGGATGTGAGGGCGCAGCTGCGGCGGTGCAGAGGAGAG 621
QY 297 sIleCysLysIleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisVa 317
DB 622 GACGTGCAGAGTGTGCTGGAACGCGCGCTGTGCATGTCTTGTGCGCGTGCAGACCT 681
QY 317 lValAlaCysAlaLysCysAlaLeuSerThrAspLysCysPrometCysArgArgThrPh 337
DB 682 GGTC--TGTGCTGAGTGTGCCCCCGGCTGACGCTGTGCCCATCTGCAGAGCCCCCGT 738
QY 337 eThrAsnAlaValArgLeuTyrPheSer 346
DB 739 CCGCAGCCCGGTGCGCAGCTTCTCTGCC 766

RESULT 2

US-11-135-855-21
; Sequence 21, Application US/1135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.1.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708

; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-21

Alignment Scores:
Pred. No.: 2.56e-23 Length: 1068
Score: 326.00 Matches: 89
Percent Similarity: 36.54% Conservative: 44
Best Local Similarity: 24.45% Mismatches: 104
Query Match: 17.28% Indels: 128
DB: 7 Gaps: 10

US-10-041-859A-2 (1-346) x US-11-135-855-21 (1-1068)

QY 102 LeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrpVal 121
DB 1 ATGGGACCTAAAGACAGTGCCTGAGTGCCTGACCGTGAACACAGCCGAGCCACTGGGCA 60
QY 122 GluGlyAspAspProAlaAlaAspHisArgArgTrpAlaPro-----GlnCys 137
DB 61 GCCGGTGATGTCCTCCACGAGAG--CGCTG-TGGACCCCGCTCTGTGGGCAGCCCTGT 116
QY 138 Pro-----PheValArgLysGlnMetTyrAlaAsnAlaGlyGlu 151
DB 117 CCTAGGCTTGACACCTGACAGACCTGGAGCCAGTGATGGGCAATCTGGGCCAGCT 176
QY 152 AlaThr-----AlaValGlyArg-AspGluCysGlyAlaSerAlaAlaThrGlnProPr 169
DB 177 GCGGCCCCGTACAGAGAGAGAGAGAGAGGCGCGGGGCCACCTTGTTCAGGGGCC 236
QY 169 oArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPh 189
DB 237 TGCCTTCCCCGGC-----ATGGGCTGTGAGAGAGTTGCGTGTGCTGCCCTCTT 281
QY 189 eLysAspTrpProArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGlyPhePh 209
DB 282 CTATGACTGGCCGCTGACTGCTGAGGTGCCACCCGAGCTGTGCTGTGCTGCCGCTTCTT 341
QY 209 eTyrThrGlyGlnGlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLysAspTr 229
DB 342 CCACACAGGCCATCAGACAGAGTGAGTGTCTTCTTGTCTATGGGGCGCTGCAGAGCTG 401
QY 229 pGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAlaTyrVa 249
DB 402 GAAGCGCGGAGCAGCCCTGAGCGGAGCATGCCAAGTGTTCCCGAGCTGTCAAGTTCTT 461
QY 249 LglLeuValLysGlyArgAspTyrIleGlnLysVal----- 261
DB 462 GCTCCGGTCAAAAGAGAGACTTGTTCACAGTGTGCAGAGAGACTCACTCCAGCTGCT 521
QY 261 ----- 261
DB 522 GGGCTCCTGGGTGAGCGCCACCTCTCTCGGGGCTCCGGGTGCGAGTGGGCTCGCCCC 581
QY 261 ----- 261
DB 582 TCCTATTTCCTCAAGGCTGATGCTCTGCTCCTTCCAGAGCCGTGGGAAGAACCGG 641
QY 262 -----LysSerGluAlaTh 266
DB 642 AAGACGAGCCCTGTGGCCCCCTCCGGTCCAGTCTGAAGTGTCCAGAGGACGAGGTGCA 701

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 26, 2005, 19:40:17 ; Search time 942 Seconds
(without alignments)
3037.372 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKPCNCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10041859 @CGN 1 1 1026 @runat_23112005_100429_13224 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	3773	5	US-10-041-859-1
2	787	41.7	50000	8	US-10-706-635-23
3	748	39.6	794	8	US-10-706-635-4
4	719.5	38.1	1317	7	US-10-267-502-202
5	719.5	38.1	1858	10	US-11-097-143-28832
6	719.5	38.1	2013	10	US-11-097-143-12365
7	719.5	38.1	10432	10	US-11-097-143-12364

8	719.5	38.1	14250	10	US-11-097-143-28831	Sequence 28831, A
9	526.5	27.9	2563	6	US-10-305-720-1076	Sequence 1076, Ap
10	526.5	27.9	2563	7	US-10-641-643-894	Sequence 894, App
11	526.5	27.9	2563	9	US-10-485-225-63	Sequence 63, Appl
12	526.5	27.9	2601	6	US-10-232-286-3	Sequence 3, Appli
13	526.5	27.9	2601	8	US-10-934-717-3	Sequence 3, Appli
14	526.5	27.9	3076	3	US-09-954-456-1635	Sequence 1635, Ap
15	526.5	27.9	3076	3	US-09-954-531-16	Sequence 16, Appl
16	526.5	27.9	3076	5	US-10-197-290-1	Sequence 1, Appli
17	526.5	27.9	3076	6	US-10-388-263-157	Sequence 157, App
18	526.5	27.9	3076	7	US-10-776-827-11	Sequence 11, Appl
19	526.5	27.9	3076	9	US-10-843-641A-1083	Sequence 1083, Ap
20	526.5	27.9	3076	9	US-10-843-641A-4662	Sequence 4662, Ap
21	526.5	27.9	3076	10	US-11-048-271-1	Sequence 1, Appli
22	526.5	27.9	3164	6	US-10-141-618-5	Sequence 5, Appli
23	526.5	27.9	3165	6	US-10-269-909-5	Sequence 5, Appli
24	526.5	27.9	3165	6	US-10-172-118-564	Sequence 564, App
25	526.5	27.9	3165	6	US-10-366-307-5	Sequence 5, Appli
26	526.5	27.9	3165	7	US-10-342-887-564	Sequence 564, App
27	526.5	27.9	5212	8	US-10-825-282-39	Sequence 39, Appl
28	526.5	27.9	5847	3	US-09-971-392-253	Sequence 253, App
29	526.5	27.9	5857	6	US-10-247-671-18	Sequence 18, Appl
30	525.5	27.8	2673	8	US-10-482-952-2	Sequence 2, Appli
31	525.5	27.8	2676	3	US-09-974-592-11	Sequence 11, Appl
32	525.5	27.8	6669	3	US-09-974-592-5	Sequence 5, Appli
33	525.5	27.8	6669	7	US-10-636-065-230	Sequence 230, App
34	524.5	27.8	1815	9	US-10-975-974-53	Sequence 53, Appl
35	524.5	27.8	2676	3	US-09-201-936-5	Sequence 5, Appli
36	524.5	27.8	2676	7	US-10-636-065-220	Sequence 220, App
37	524.5	27.8	2676	7	US-10-600-272-5	Sequence 5, Appli
38	524.5	27.8	2916	7	US-10-240-425-1436	Sequence 1436, Ap
39	524.5	27.8	2916	7	US-10-776-827-31	Sequence 31, Appl
40	517.5	27.4	2450	3	US-09-201-936-39	Sequence 39, Appl
41	517.5	27.4	2474	7	US-10-636-065-226	Sequence 226, App
42	517.5	27.4	2474	7	US-10-600-272-39	Sequence 39, Appl
43	514.5	27.3	3153	8	US-10-482-952-10	Sequence 10, Appl
44	507.5	26.9	1857	9	US-10-975-974-47	Sequence 47, Appl
45	507.5	26.9	2580	3	US-09-201-936-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-041-859-1
; Sequence 1, Application US/10041859
; Publication No. US20030049796A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, QIHONG
; APPLICANT: REED, JOHN C.
; APPLICANT: DEVERAUX, QUINN L.
; APPLICANT: MAEDA, SUSUMU
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
; FILE REFERENCE: 087102/027 2537
; CURRENT APPLICATION NUMBER: US/10/041, 859
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,478
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3773
; TYPE: DNA
; ORGANISM: Bombyx mori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2733)..(3770)
US-10-041-859-1

Alignment Scores:
Pred. No.: 1.84e-208 Length: 3773
Score: 1887.00 Matches: 346
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-10-041-859A-2 (1-346) x US-10-041-859-1 (1-3773)

QY	1	MetGlLeuThrLysValAlaLysAsnGlyAlaAlaThrLeuValMetLeuLysAsn	20
DB	206	ATGGAAGTTGACGAAAGTTGCTAAATAATGAGCTGCCGCCAGTTGGTGAATTTAAAAAT	265
QY	21	AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer	40
DB	266	GCGCGGATGCAAAAATGCGACCTTTTCATTGGTCCGCTCATGTTATCCTCGTGTAGTCT	325
QY	41	SerThrThrSerThrLeuProSerProSerSerSerAlaAspLysThrAspAsnHisAsp	60
DB	326	TCAACGACATCCACACTCCCGTCACCTTCGTCTCAGCTGATAAAACGGATATCAAGAC	385
QY	61	ThrPheAsnPhelLeuProAspMetProAspMetArgArgGluGluLysThr	80
DB	386	ACATTCAACTTCCTTCTCTGATATGCCCGACATGCGTGTGAAGAAGAACGTTGAAAAACA	445
QY	81	PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr	100
DB	446	TTTGATCAGTGCCCGTTACGTTTGTGACGCCGGAACAATTGCCCGCAACGGATTCTAC	505
QY	101	TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrp	120
DB	506	TACCTCGGTCCGGCGACGAAGTGTGCTGTCTTCTGTAAAGGTAGAAATTATGAGTGG	565
QY	121	ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal	140
DB	566	GTCGAAGCGCAGCATCCTCGCGCGATCATCGAGATGGCGCCCAAGTGTCCCTTGTGA	625
QY	141	ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys	160
DB	626	CGAAAACAATGTATGCCAACGCTGGGGAGAGGCGACCGCTGTCCGTAGAGACGAATGT	685
QY	161	GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer	180
DB	686	GGGGCCAGTGGCGCCACCGCAGCTCCCGCATGCCCCGCCGCTGCACGCCGGTACTCC	745
QY	181	ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro	200
DB	746	ACCGAGGCGCGCGCTGCCACCTTCAAGACTGGCCGAGAAGCCTATGCCCAAAACC	805
QY	201	GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe	220
DB	806	GAGGAAGTGCAGAGGCGCGGATCTTCTATACAGGCCAAGGTGACAAAAAGAAATGCTTC	865
QY	221	TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla	240
DB	866	TATTGCGACGAGGGCTAAAGATTGGGAAGCGATGCTCCGTGGGAACAGACGCC	925
QY	241	ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys	260
DB	926	AGATGGTTCGACCGCTGCCGTAAGTGCATTTGGTGAAGAAGCAGTACTACATTCAGAAAG	985
QY	261	ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGlnAlaAlaThrAsnAsp	280
DB	986	GTGAAGTCGAGGCCACTGCGATATCTGCTAGCGAAGAAACAAGGCCGCCACCAATGAT	1045
QY	281	SerThrLysAsnValAlaGlnGluGlyGlyLysHisLeuAspAspSerLysIleCysLys	300
DB	1046	TGCACTAAGAACGTGCGCCCAAGAGGGCGAGAAAACATTTGATGACTCTAAATAATGTAAA	1105
QY	301	IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValAlaLysCys	320
DB	1106	ATATGTATTCCGAGAGCGTAACGTGTGCTTCGTGCCGTGCGGCCACGTTGGCGGTGC	1165
QY	321	AlaLysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAla	340
DB	1166	GCCAAAGTGGCGCTGTGCACGCAAGTAGTCCCGATGTGTCCAGGACGTTACGAAATGCCG	1225

QY 341 ValArgLeuTyrPheSer 346
DB 1226 GTGCGGCTTACTTCTCG 1243

RESULT 2
US-10-706-635-23/C
; Sequence 23, Application US/10706635
; Publication No. US20050014263A1
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; FILE REFERENCE: US-221C1XCZ1
; CURRENT APPLICATION NUMBER: US/10/706,635
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/662,254
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Amsacta moorei entomopoxvirus
US-10-706-635-23

Alignment Scores:
Pred. No.: 7,49e-79 Length: 50000
Score: 787.00 Matches: 143
Percent Similarity: 63.82% Conservative: 44
Best Local Similarity: 48.81% Mismatches: 86
Query Match: 41.71% Indels: 20
DB: 8 Gaps: 5

US-10-041-859A-2 (1-346) x US-10-706-635-23 (1-50000)

QY	55	LysThrAspAsnHisAspThrPheAsnPhelLeuProAspMetProAspMetArg-----	72
DB	24584	AAAATAACATACATATATATATTTATATAATATGATGATGACATTAACCTGTAT	24525
QY	73	ArgGluGluGluArgLeuLysThrPheAspGlnTrpProValThrPheLeuThrProGlu	92
DB	24524	AATGAATCTGAAGATTACAACATTTGAAATGGCCCATTAATTTTATACTCCTGAA	24465
QY	93	GlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCysAlaPhe	112
DB	24464	TCATTGTCTAGTAATGGAATTTATATATAGGTGAGAATGATACAGTTAAATGTGTAT	24405
QY	113	CysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHisArgArg	132
DB	24404	TGTGAGTACAAATAAATAATGAGGTGAAGCGATTAAACAGAAATTGATCAATAAAAA	24345
QY	133	TrpAlaProGlnCysProPheValArgLysGlnMetTyrAlaAsnAlaGlyGluAla	152
DB	24344	TTTTCTCCAATGTAGTTTTTAAATCTAAT-----	24312
QY	153	ThrAlaValGlyArgAspGluCysGlyAlaSerAlaAlaThrGlnProProArgMetPro	172
DB	24311	-----GATGAATAGATGAGTGTGCGCAATATAAAATATATCTAACATTACACAAAAA	24258
QY	173	GlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPheLysAspTrp	192
DB	24257	GGAGCAGTTCAATCTTAATCTATCAAAATATTGTTGAAAAGACTTAAACATATAAAGAGTGG	24198
QY	193	ProArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGlyPhePheTyrThrGly	212
DB	24197	CCTATTTCATGCTTATTCTACAGAAAACTAGCAAGCTGGAATTCCTTTATTACTGGA	24138



GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 26, 2005, 17:44:57 ; Search time 225 Seconds
(without alignments)
2733.495 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B COMB.seq: *
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7: /cgn2_6/ptodata/1/ina/PP COMB.seq: *
8: /cgn2_6/ptodata/1/ina/RE COMB.seq: *
9: /cgn2_6/ptodata/1/ina/backfilese1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C	787	41.7	50000	3	US-09-662-254B-23
4	748	39.6	794	3	US-09-662-254B-4
5	725.5	38.4	1317	3	US-09-586-305A-2
6	723.5	38.3	1317	3	US-09-586-305A-1
7	723.5	38.3	1317	3	US-09-586-305A-3
8	717.5	38.0	1317	3	US-09-586-305A-4
9	717.5	38.0	1317	3	US-09-586-305A-5

10	715.5	37.9	1317	3	US-09-586-305A-9	Sequence 9, Appli
11	713.5	37.8	1317	3	US-09-586-305A-10	Sequence 10, Appl
12	712.5	37.8	1317	3	US-09-586-305A-6	Sequence 6, Appli
13	712.5	37.8	1317	3	US-09-586-305A-7	Sequence 7, Appli
14	704	37.3	1304	3	US-09-586-305A-8	Sequence 8, Appli
15	526.5	27.9	2563	3	US-09-016-434-1076	Sequence 1076, Ap
16	526.5	27.9	2563	3	US-09-023-655-894	Sequence 894, App
17	526.5	27.9	2601	3	US-08-569-749-3	Sequence 3, Appli
18	526.5	27.9	2601	3	US-09-689-366-3	Sequence 3, Appli
19	526.5	27.9	2601	3	US-10-232-286-3	Sequence 3, Appli
20	526.5	27.9	2601	6	PCT-US96-12860-3	Sequence 3, Appli
21	526.5	27.9	3076	2	US-09-205-144-1	Sequence 1, Appli
22	526.5	27.9	3076	3	US-09-814-915A-11	Sequence 11, Appl
23	526.5	27.9	3165	3	US-09-949-016-160	Sequence 160, App
24	526.5	27.9	3573	3	US-09-949-016-5007	Sequence 5007, Ap
25	525.5	27.8	2676	3	US-08-212-971-11	Sequence 11, Appl
26	525.5	27.8	2676	3	US-08-800-929A-11	Sequence 11, Appl
27	525.5	27.8	2676	3	US-09-617-053A-11	Sequence 11, Appl
28	525.5	27.8	6669	3	US-09-212-971-5	Sequence 5, Appli
29	525.5	27.8	6669	3	US-08-800-929A-5	Sequence 5, Appli
30	525.5	27.8	6669	3	US-09-617-053A-5	Sequence 5, Appli
31	525.5	27.8	6669	3	US-09-672-717-230	Sequence 230, App
32	524.5	27.8	2676	2	US-08-511-485-5	Sequence 5, Appli
33	524.5	27.8	2676	3	US-09-201-936-5	Sequence 5, Appli
34	524.5	27.8	2676	3	US-09-011-356-5	Sequence 5, Appli
35	524.5	27.8	2676	3	US-09-672-717-220	Sequence 220, App
36	524.5	27.8	2676	3	US-09-201-932-5	Sequence 5, Appli
37	524.5	27.8	2916	3	US-09-814-915A-31	Sequence 31, Appl
38	517.5	27.4	2450	3	US-09-201-936-39	Sequence 39, Appl
39	517.5	27.4	2450	3	US-09-932-39	Sequence 39, Appl
40	517.5	27.4	2474	3	US-09-011-356-39	Sequence 39, Appl
41	517.5	27.4	2474	3	US-09-672-717-226	Sequence 226, App
42	507.5	26.9	2580	2	US-08-511-485-7	Sequence 7, Appli
43	507.5	26.9	2580	3	US-09-201-936-7	Sequence 7, Appli
44	507.5	26.9	2580	3	US-09-011-356-7	Sequence 7, Appli
45	507.5	26.9	2580	3	US-09-672-717-222	Sequence 222, App

ALIGNMENTS

RESULT 1
US-09-502-528-2
; Sequence 2, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502, 528
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: SfIAP nucleotide sequence, open reading frame
; OTHER INFORMATION: (ORF) only
; NAME/KEY: CDS
; LOCATION: (1)..(1134)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SfIAP)
US-09-502-528-2

Alignment Scores:
Pred. No.: 2.73e-129 Length: 1134
Score: 1311.00 Matches: 248
Percent Similarity: 79.28% Conservative: 39
Best Local Similarity: 68.51% Mismatches: 57

Query Match: 69.48% Indels: 18
DB: 3 Gaps: 7
US-10-041-859A-2 (1-346) x US-09-502-528-2 (1-1134)

QY 1 MetGluLeuThrIysValAlaIlyAsnGlyAlaAlaAlaThrLeuValMetLeuIysAsn 20
DB 52 ATGGATATTACCAAGGTGCATCCCAATGGCTCCTCTCAACATTAAACGCTATTCAAGAGC 111
QY 21 --AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeu-----SerSer 37
DB 112 GGATCGCTGAGGCTAAAAATTGACCT--CTCGCGCACTAATGCTGCGGACGCAAGT 168
QY 38 CysGluSerSerThrThrSerThrLeuProSerProSerSer----- 51
DB 169 TACGACTCCAAACGCGCGCTCTCCATCTTGTCTCCATCCACGCCCTTGCTTTCATCTTCT 228
QY 52 ---SerAlaAspIysThrAspAsnHisAspThrPheAsnPhelLeuProAspMetProAsp 70
DB 229 TTCTCCATTGATAAAACGACAACACGACACCTTCGCTTCAGTGCAGACAGATTGAT 288
QY 71 MetArgArgGluGluGluArgLeuIysThrPheAspGlnTrpProValThrPheLeuThr 90
DB 289 ATGAGAAAAGAGATGAACGTATGAAAACATTGAAAAATGGCCCGTAAGTTTCTATCC 348
QY 91 ProGluGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys 110
DB 349 GGAGAGCAACTTGCTCGAAATGGATTTTACTACCTCGCGCGTAGAGATGAAGCCCGTTGC 408
QY 111 AlaPheCysIysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
DB 409 GCTTCTGTAAAGTGAATTATGAGGTGGTGGAGGCGATGACCCTGCGAAGACCAT 468
QY 131 ArgArgTrpAlaProGlnCysProPheValArgIysGlnMetTyrAlaAsnAlaGlyGly 150
DB 469 CAGCGTTGGCGCCACAGTCCCATTTGTGCGCAAA--TTGAACGGTACTGCAACAGCA 525
QY 151 GluAlaThrAlaValGlyArgAspGluCysGlyAlaSerAlaAla-----ThrGln 167
DB 526 GACACGGGTAGTTCGGGCGAGAGACGAGTGTGTGCCGCGCGCTCCCTCCGGTAACCTCT 585
QY 168 ProProArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAla 187
DB 586 CCGCCGCGTATGCGCGGTCCTCGTGACCCACCGATATGCATCTGAAGCCGCACGACTACGC 645
QY 188 ThrPheIysAspTrpProArgArgMetArgGlnIysProGluGluLeuAlaGluAlaGly 207
DB 646 AGTTTAAAGACTGGCCACGATGCATGCGACAAAACTGAAAGACTCGCCGAGGCTGGC 705
QY 208 PhePheTyrThrGlyGlnGlyAspIysThrIysCysPheTyrCysAspGlyGlyLeuIys 227
DB 706 TTTTTTTACACTGGTCAAGGAGACAAAAACAAGTGTTTTATTGCGATGGTGAATTAATA 765
QY 228 AspTrpGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAla 247
DB 766 GATTGGAGAAACCATGACGTACCTTGGGAACAACACGCAAGTGTGATGACCGTTCGCC 825
QY 248 TyrValGlnLeuValIysGlyArgAspTyrIleGlnIysValIysSerGluAlaThrAla 267
DB 826 TACGTGCAATTGTTGAGGGTCAAGATACGTTCAAAAGTGATTTCTGAAGCTTGTAG 885
QY 268 IleSerAlaSerGluGluGluGln-----AlaAlaThrAsnAspSerThrIysAsn 284
DB 886 GTATCCGCGTCAGAAAGCGGAACGTGATGACACCCGCAAGGACTGCCGAGCCAAACCCG 945
QY 285 ValAlaGlnGluGlyIysHisIleuAspAspSerIysIleCysIysIleCysTyrSer 304
DB 946 CCAGCAGAGGCGCCAGAAAACTCAGTCGATGACTCAAGTTGTGTAAATCTGTATGCT 1005
QY 305 GluGluArgAsnValCysPheValProCysGlyHisValValAlaCysAlaIysCysAla 324
DB 1006 GAAGAGCGTAACGTGTGTGCTGTCGCGCGCACGCTGTGGCTTGCGCCAAGTGGCGG 1065

QY 325 LeuSerThrAspIysCysPrometCysArgArgThrPheThrAsnAlaValArgLeuTyr 344
DB 1066 CTGGCGCGCCAGCAAGTCCCCCATGTGCGCGCAGACAGCTTCAAAATGACAGTGGTTATAT 1125
QY 345 PheSer 346
DB 1126 TTCTCG 1131

RESULT 2

US-09-502-528-1
; Sequence 1, Application US/09502528
; Patent No. 6570069
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; APPLICANT: Huang, Qihong
; APPLICANT: Maeda, Susumu
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Inhibitors of Apoptosis
; FILE REFERENCE: 023070-112000US
; CURRENT APPLICATION NUMBER: US/09/502,528
; CURRENT FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Spodoptera frugiperda
; FEATURE:
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SFIAP) nucleotide sequence including 5' and 3'
; OTHER INFORMATION: untranslated regions, full length SFIAP cDNA
; NAME/KEY: CDS
; LOCATION: (229)..(1362)
; OTHER INFORMATION: fall armyworm inhibitor of apoptosis protein
; OTHER INFORMATION: (SFIAP)
US-09-502-528-1

Alignment Scores:
Pred. No.: 5.18e-129 Length: 1739
Score: 1311.00 Matches: 248
Percent Similarity: 79.28% Conservative: 39
Best Local Similarity: 68.51% Mismatches: 57
Query Match: 69.48% Indels: 18
DB: 3 Gaps: 7

US-10-041-859A-2 (1-346) x US-09-502-528-1 (1-1739)

QY 1 MetGluLeuThrIysValAlaIlyAsnGlyAlaAlaAlaThrLeuValMetLeuIysAsn 20
DB 280 ATGGATATTACCAAGGTGCATCCCAATGGCTCCTCTCAACATTAAACGCTATTCAAGAGC 339
QY 21 --AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeu-----SerSer 37
DB 340 GGATCGCTTGAGGCTAAAAATTGACCT--CTCGCGCACTAATGCTGCGGACGCCAAGT 396
QY 38 CysGluSerSerThrThrSerThrLeuProSerProSerSer----- 51
DB 397 TACGACTCCAAACGCGCGCTCTCCATCTTGTCTCCATCCACGCCCTTGCTTTCATCTTCT 456
QY 52 ---SerAlaAspIysThrAspAsnHisAspThrPheAsnPhelLeuProAspMetProAsp 70
DB 457 TTCTCCATTGATAAAACGACAACACGACACCTTCGGCTTCAGTGCAGACAGATTGAT 516
QY 71 MetArgArgGluGluGluArgLeuIysThrPheAspGlnTrpProValThrPheLeuThr 90
DB 517 ATGAGAAAAGAGATGAACGTATGAAAAACATTGAAAAATGGCCCGTAAGTTTCTATCC 576
QY 91 ProGluGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys 110
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QY 111 AlaPheCysIysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 26, 2005, 17:43:32 ; Search time 4719 Seconds
(without alignments)
3430.458 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 segs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_est3:*
4: gb_hlc:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	1053	55.8	727	3	BP120885	BP120885 BP120885
3	985	52.2	723	1	AV401669	AV401669 AV401669
4	928	49.2	622	7	CK497882	CK497882 rswb0_00
5	861.5	45.7	555	3	BP121882	BP121882 BP121882
6	812	43.0	512	1	AV398511	AV398511 AV398511
7	709.5	37.6	624	7	CV526245	CV526245 He_wd1_09

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	9	647	34.3	804	10	CG786123	CG786123 CM_MBA-76
	10	545	28.9	892	8	CV838287	CV838287 ID0ACC7CC
	11	545	28.9	1277	4	CNS0FU4S	CR688416 Tetraodon
	12	536	28.4	1328	4	CNS0FWYZ	CR692095 Tetraodon
	13	520	27.6	1334	4	CNS0GPM3	CR729221 Tetraodon
	14	519	27.5	522	7	CK516014	CK516014 rswjb0_00
	15	514	27.2	723	7	CO640316	CO640316 USDA-FP_1
	16	510.5	27.1	1778	10	AY420755	AY420755 Mus muscu
	17	503	26.7	2030	4	CNS0GT10	CR733861 Tetraodon
	18	500.5	26.5	782	6	CB690915	CB690915 Cy23 Aede
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	20	497	26.3	1428	4	CNS0G4NH	CR702049 Tetraodon
	21	493.5	26.2	1799	10	AY420753	AY420753 Homo sapi
	22	488	25.9	2037	4	CNS0GLWG	CR724410 Tetraodon
	23	486	25.8	1851	4	BC056914	BC056914 Homo sapi
	24	468.5	24.8	1133	8	DN682800	DN682800 CGX26-C05
	25	467	24.7	864	7	CK189215	CK189215 EST778530
	26	465	24.6	2632	4	CR859301	CR859301 Pongo pyg
	27	453.5	24.0	718	4	AY432429	AY432429 Aedes aeg
	28	447.5	23.7	786	8	DR832669	DR832669 JGI_CABC2
	29	447	23.7	890	8	CX414917	CX414917 JGI_XZT56
	30	446.5	23.7	887	7	CNS02150	CNS02150 AGENCOURT
	31	446	23.6	771	6	CA803224	CA803224 ESG011a.E
	32	445.5	23.6	871	8	DN012763	DN012763 JGI_CAAQ1
	33	445	23.6	727	6	CF525095	CF525095 AGENCOURT
	34	445	23.6	788	8	DN069067	DN069067 JGI_CABD5
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	37	444	23.5	878	8	CX498117	CX498117 JGI_XZG43
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	41	438.5	23.2	898	8	CV814302	CV814302 AGENCOURT
	42	438.5	23.2	918	8	DN039298	DN039298 JGI_CAAR1
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	44	435	23.1	886	5	BQ652590	BQ652590 AGENCOURT
	45	434.5	23.0	580	3	BP292682	BP292682 BP292682

ALIGNMENTS

RESULT 1
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LOCUS BP121000 cen- Bombyx mori cDNA clone cen-4016, mRNA sequence.
DEFINITION BP121000
ACCESSION BP121000
VERSION BP121000.1 GI:29554042
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 712)
Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cDNA (Mita,K. 2003)
Unpublished (2003)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6121
Email: kmita@nias.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3').

FEATURES

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/mol_type="mRNA"
/db_xref="taxon:7091"
/clone="cen-4016"

/cissue_type="compound eye"
/clone_lib="cen-"
/note="mixed stages from 5th instar larva to pupa"

ORIGIN

Alignment Scores:

Pred. No.:	9.91e-96	Length:	712
Score:	1053.00	Matches:	192
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	55.80%	Indels:	0
DB:	3	Gaps:	0

US-10-041-859A-2 (1-346) x BP121000 (1-712)

QY	154	AlaValGlyArgAspGluCysGlyAlaSerAlaAlaThrGlnProProArgMetProGly	173
DB	1	GCTGTCGTAAGACGAATGTGGGCCAGTGC GGCCACGCACTCTCCCGCATGCCCGC	60
QY	174	ProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPheLysAspTrpPro	193
DB	61	CCCGTGACGCGCGTACTCCACCGAGCCGCGGCTCGCCACCTTCAAGGACTGGCCG	120
QY	194	ArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGln	213
DB	121	AGATGTATGCCCAAAACCCGAGAACTGCGAGAGCGCGGATTTCTTATACAGGCCAA	180
QY	214	GlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLysAspTrpGluSerAspAsp	233
DB	181	GGTGACAAACGAATGCTTCTATTGCGACGGAGGGCTAAAGATTGGGAAGCGATGAC	240
QY	234	ValProTrpGluGlnHisAlaArgTrpPheAspArgCysAlaTyrValGlnLeuValLys	253
DB	241	GTTCCGTGGGAACAGCACGCCAGATGGTTCGACCGCTGCGCTGACGTCAATTGGTGAA	300
QY	254	GlyArgAspTyrIleGlnLysValLysSerGluAlaThrAlaIleSerAlaSerGluGlu	273
DB	301	GGACGTGACTACATTCAGAAAGTGAAGTCGAGGCCACTGCATATCTGTAGCGAAAGA	360
QY	274	GluGlnAlaAlaThrAsnAspSerThrLysAsnValAlaGlnGluGlyLysHisLeu	293
DB	361	GAAACAGGCCGCCACCAATGATTCGACTAAGAACGTCGCTCAAGAGGCGAAGAACATTG	420
QY	294	AspAspSerLysIleCysLysIleCysTyrSerGluGluArgAsnValCysPheValPro	313
DB	421	GATGACTCTAAATATGTAAATATATGTATTCCGAGGAGCGCTAACGTGTGTCGCCG	480
QY	314	CysGlyHisValValAlaCysAlaLysCysAlaLeuSerThrAspLysCysPrometCys	333
DB	481	TGCGGCCACGTGGTGGCGTCGCCAAGTGC GCGCTGTGACGAGCAAGTGC CGATGTGT	540
QY	334	ArgArgThrPheThrAsnAlaValArgLeuTyrPheSer	346
DB	541	CGCAGGACGTTACGAATGCGGTGCGGCTTACTTCTCG	579

RESULT 2
BP120885 727 bp mRNA linear EST 16-MAY-2003
LOCUS BP120885 cen- Bombyx mori cDNA clone cen-3830, mRNA sequence.
DEFINITION BP120885
ACCESSION BP120885
VERSION BP120885.1 GI:29553920
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori

REFERENCE
AUTHORS Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
TITLE Bombyx mori cDNA (Mita,K. 2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Mita K
Genome Research Group

National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Tel: 81-29-838-6120
Fax: 81-29-838-6121
Email: kmita@nias.affrc.go.jp
method: uni-directional, sequence direction: sequenced from T3 primer
(5' -> 3').

FEATURES

source

Location/Qualifiers
1. 727
/organism="Bombyx mori"
/mol_type="mRNA"
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/cissue_type="compound eye"
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/note="mixed stages from 5th instar larva to pupa"

ORIGIN

Alignment Scores:

Pred. No.:	1.02e-95	Length:	727
Score:	1053.00	Matches:	192
Percent Similarity:	99.48%	Conservative:	0
Best Local Similarity:	99.48%	Mismatches:	1
Query Match:	55.80%	Indels:	0
DB:	3	Gaps:	0

US-10-041-859A-2 (1-346) x BP120885 (1-727)

QY	154	AlaValGlyArgAspGluCysGlyAlaSerAlaAlaThrGlnProProArgMetProGly	173
DB	1	GCTGTCGTAAGACGAATGTGGGCCAGTGC GGCCACGCACTCTCCCGCATGCCCGC	60
QY	174	ProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPheLysAspTrpPro	193
DB	61	CCCGTGACGCGCGTACTCCACCGAGCGCGGCTCGCCACCTTCAAGGACTGGCCG	120
QY	194	ArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGln	213
DB	121	AGATGTATGCCCAAAACCCGAGAACTGCGAGAGCGGCTTCTTATACAGGCCAA	180
QY	214	GlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLysAspTrpGluSerAspAsp	233
DB	181	GGTGACAAACGAATGCTTCTATTGCGACGGAGGCGCTAAAGATTGGGAAGCGATGAC	240
QY	234	ValProTrpGluGlnHisAlaArgTrpPheAspArgCysAlaTyrValGlnLeuValLys	253
DB	241	GTTCCGTGGGAACAGCACGCCAGATGGTTCGACCGCTGCGCTGACGTCAATTGGTGAA	300
QY	254	GlyArgAspTyrIleGlnLysValLysSerGluAlaThrAlaIleSerAlaSerGluGlu	273
DB	301	GGACGTGACTACATTCAGAAAGTGAAGTCGAGGCCACTGCATATCTGTAGCGAAGAA	360
QY	274	GluGlnAlaAlaThrAsnAspSerThrLysAsnValAlaGlnGluGlyLysHisLeu	293
DB	361	GAAACAGGCCGCCACCAATGATTCGACTAAGAACGTCGCTCAAGAGGCGAAGAACATTG	420
QY	294	AspAspSerLysIleCysLysIleCysTyrSerGluGluArgAsnValCysPheValPro	313
DB	421	GATGACTCTAAATATGTAAATATATGTATTCCGAGGAGCGTAACTGTGTCGCCG	480
QY	314	CysGlyHisValValAlaCysAlaLysCysAlaLeuSerThrAspLysCysPrometCys	333
DB	481	TGCGGCCACGTGGTGGCGTCGCCAAGTGC GCGCTGTGACGAGCAAGTGC CGATGTGT	540
QY	334	ArgArgThrPheThrAsnAlaValArgLeuTyrPheSer	346
DB	541	CGCAGGACGTTACGAATGCGGTGCGGCTTACTTCTCG	579

RESULT 3
AV401669 723 bp mRNA linear EST 01-MAR-2005
LOCUS AV401669
DEFINITION AV401669 Bombyx mori C108 splinling stage day-0 Bombyx mori cDNA
clone hes00025 T3, mRNA sequence.

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 26, 2005, 17:39:37 ; Search time 714 Seconds
(without alignments)
3229.669 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFTO_spool/US10041859/runat_23112005_100426_13104/app_query.fasta_1.519
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10041859 @CGN 1_1_727 @runat_23112005_100426_13104 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21: *
1: geneseqn19808: *
2: geneseqn19908: *
3: geneseqn20008: *
4: geneseqn20018: *
5: geneseqn20018s: *
6: geneseqn20028: *
7: geneseqn20028s: *
8: geneseqn20038: *
9: geneseqn20038s: *
10: geneseqn20038s: *
11: geneseqn20038s: *
12: geneseqn20048: *
13: geneseqn20048s: *
14: geneseqn20058: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1887	100.0	3773	6	ABQ78228 Nucleotid
2	1311	69.5	1739	5	AAD14419 Fall army
3	787	41.7	5000	6	ABL55643 AMEPV gen
4	748	39.6	794	6	ABL55635 AMEPV bac

5	721.5	38.2	1317	5	AAC84521	Aac84521 Drosophil
6	719.5	38.1	1317	5	AAC84520	Aac84520 Drosophil
7	719.5	38.1	1317	5	AAC84522	Aac84522 Drosophil
8	719.5	38.1	1317	12	ADO07876	Ado07876 Fly polyn
9	719.5	38.1	1858	4	ABL21061	Abi21061 Drosophil
10	719.5	38.1	2013	4	ABL10083	Abi10083 Drosophil
11	719.5	38.1	10432	4	ABL10082	Abi10082 Drosophil
12	719.5	38.1	14250	4	ABL21060	Abi21060 Drosophil
13	713.5	37.8	1317	5	AAC84523	Aac84523 Drosophil
14	713.5	37.8	1317	5	AAC84524	Aac84524 Drosophil
15	711.5	37.7	1317	5	AAC84528	Aac84528 Drosophil
16	709.5	37.6	1317	5	AAC84529	Aac84529 Drosophil
17	708.5	37.5	1317	5	AAC84525	Aac84525 Drosophil
18	708.5	37.5	1317	5	AAC84526	Aac84526 Drosophil
19	700	37.1	1304	5	AAC84527	Aac84527 Drosophil
20	546.5	29.0	131680	10	ADF29092	Adf29092 Agrotis s
21	526.5	27.9	2563	9	ADB80989	Adb80989 RING-SH c
22	526.5	27.9	2563	10	ACA56478	Acas6478 Human sig
23	526.5	27.9	2563	11	ADI31568	Adi31568 Human CDN
24	526.5	27.9	2563	12	ADI56274	Adi56274 Human pol
25	526.5	27.9	2563	13	ADS83635	Ads83635 Human lym
26	526.5	27.9	2601	2	AAT61591	Aat61591 Human c-I
27	526.5	27.9	3076	2	AAT72712	Aat72712 Human inh
28	526.5	27.9	3076	2	AAZ41005	Aaz41005 Human cel
29	526.5	27.9	3076	2	AAZ22096	Aaz22096 Human cel
30	526.5	27.9	3076	6	ABL62746	Abi62746 Breast ca
31	526.5	27.9	3076	6	ABL66325	Abi66325 Lung canc
32	526.5	27.9	3076	8	ABX10968	Abx10968 CDNA enco
33	526.5	27.9	3076	10	AAD60472	Aad60472 Human cel
34	526.5	27.9	3164	8	ABV75363	Abv75363 Human CIA
35	526.5	27.9	3164	12	ADG87134	Adg87134 Human CIA
36	526.5	27.9	3165	12	ADH74642	Adh74642 CDNA enco
37	526.5	27.9	3165	13	ADR24703	Adr24703 Breast ca
38	526.5	27.9	3165	13	ADR67123	Adr67123 Human bla
39	526.5	27.9	5212	8	ABX10333	Abx10333 DNA enco
40	526.5	27.9	5212	13	ADU22898	Adu22898 Human apo
41	526.5	27.9	5243	14	AEB22769	Aeb22769 Human col
42	526.5	27.9	5844	10	ADB47553	Adb47553 Human CDN
43	526.5	27.9	5857	10	ADE25614	Ade25614 Human CDN
44	525.5	27.8	2673	8	ABZ58100	Abz58100 Mouse inh
45	525.5	27.8	2676	2	AAV55042	Aav55042 Murine HI

ALIGNMENTS

RESULT 1	
ABQ78228	
ID	ABQ78228 standard; cDNA; 3773 BP.
XX	
AC	ABQ78228;
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	Nucleotide sequence of inhibitor of apoptosis protein BmiAP.
XX	
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;
XX	
KW	Spodoptera frugiperda; insult-resistant plant; caspase; gene; ss.
XX	
OS	Bombyx mori.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	2733..3773
FT	/*tag= a
XX	/product= "inhibitor of apoptosis protein BmiAP"
XX	
PN	WO200253586-A2.
XX	
PD	11-JUL-2002.
XX	
PF	07-JAN-2002; 2002WO-US000314.
XX	
PR	08-JAN-2001; 2001US-0260478P.
XX	

PA (BURN-) BURNHAM INST.
XX
PI Maeda S, Huang Q, Reed JC, Deveraux QL;
XX WPI; 2002-590628/63.
DR P-PSDB; ABB78046.

XX Novel recombinant polypeptide, inhibitor of apoptosis protein family
PT member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting
PT apoptosis and identifying an agent that modulates activity of
PT polypeptide.

XX Claim 8; Page 29-30; 62pp; English.

XX The present scone encodes a polypeptide which is an inhibitor of
CC apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is
CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC mori cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insult-resistant plant. BmiAP is also
CC useful for inhibiting caspases

XX Sequence 3773 BP; 1108 A; 785 C; 866 G; 1014 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.58e-168 Length: 3773
Score: 1887.00 Matches: 346
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-041-859A-2 (1-346) x ABQ78228 (1-3773)

QY 1 MetGluLeuThrIyValAlaIyAsnGlyAlaAlaThrLeuValMetLeuIyAsn 20
DB 206 ATGAGTTGACGAAAGTTCTAAAAATGAGCTGCCCAAGTTGGTATGTTAAAAAT 265
QY 21 AlaArgAspAlaIyMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer 40
DB 266 GCGCGGATGCAGAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGAAGTCT 325
QY 41 SerThrThrSerThrLeuProSerProSerSerSerAlaAspLySThrAspAsnHisAsp 60
DB 326 TCAACGACATCCACACTCCCGTCACCTTCGTCGCTGATATAAAGGATATCACGAC 385
QY 61 ThrPheAsnPhelEuProAspMetProAspMetArgGluGluIyAspGlySerThr 80
DB 386 ACATTCAACTCTCTCTGATATGCCCGACATGCGTCGTGAAGAGAACGTGCAAAACA 445
QY 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr 100
DB 446 TTTGATCAGTGGCCCGTTACGTTTGTGACGCCGGAACAATGGCCCCGCAAGATTCTAC 505
QY 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysIyValGluIleMetArgTrp 120
DB 506 TACCTCGGTCCGCGCGCAAGTGTGCTGTCTTCTGTAAAGTAGAAATATGAGGTGG 565
QY 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140
DB 566 GTCGAAGCGCAGCATCTCGCCGCGATCATCGAGATGGGCGCCCGAGTGTCTTTGTA 625
QY 141 ArgIySGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValAlaGlyAspGluCys 160
DB 626 CGAAAAACAATGTATGCCAACGCTGGGGAGAGAGCGACCGCTGTGCTAGAGACGAATGT 685
QY 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180
DB 686 GGGGCCAGTGGCGCCACGACCTCCCGCATGCCCGCCCGTGCACGCCGGGTACTCC 745
QY 181 ThrGluAlaAlaArgLeuAlaThrPheIyAspTrpProArgMetArgGlnIyAspPro 200

DB 746 ACCGAGCGCGCGGCTCGCCACCTTCAAGACTGGCCGAGACGTTATGCCCAAAACC 805
QY 201 GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLySThrIyS CysPhe 220
DB 806 GAGAACTGGCAGAGCGCCGATTCTTTATACAGGCCCAAGGTGACAAAAAGAAATGCTTC 865
QY 221 TyrCysAspGlyGlyLeuIyAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
DB 866 TATTGCGACGAGGGCTAAAGATTTGGGAAAGCATGACGTTCCGTGGGAACAGACGCC 925
QY 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValIySGlyArgAspTyrIleGlnIyS 260
DB 926 AGATGTTCCAGCCGCTGCCGCTACGTCATTTGGTGAAGAGCGTGACTACATTACAGAG 985
QY 261 ValIySGerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAsnAsp 280
DB 986 GTGAAGTCGAGGCCACTGCGATATCTGTACCGAAGAAACAGGCCCCCAACCAATGAT 1045
QY 281 SerThrIyAsnValAlaGlnGluGlyGluIySHisLeuAspAspSerIySileCysIyS 300
DB 1046 TCGACTAAGAACGTCGCCCAAGAGGGCGGAGAAACATTGGATGACTTTAAATATGTAAA 1105
QY 301 IleCysTyrSerGluGluArgAsnValCysPheValProCysSGlyHisValAlaCys 320
DB 1106 ATATGTTATTCGAGAGACGTTAACGTGTCTTCGTGCCGTGCCGCCACGTGTGGCGTGC 1165
QY 321 AlaIySGysAlaLeuSerThrAspLySGysPrometCysArgArgThrPheThrAsnAla 340
DB 1166 GCCAAGTGGCGGTGTGCGACGACCAAGTCCCGATGTGTGCGAGAGCGTTCACGAATGCG 1225
QY 341 ValArgLeuTyrPheSer 346
DB 1226 GTGCGGCTTACTTCTCG 1243

RESULT 2
AADI4419
ID AADI4419 standard; cDNA; 1739 BP.
XX AADI4419;
AC
XX
DT 01-NOV-2001 (first entry)
XX
DE Fall armyworm inhibitor of apoptosis (IAP) cDNA.
XX
KW Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW myocardial infarction; stroke; reperfusion injury; cancer; nootropic;
KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW neuroprotective; antianaemic; cardiant; cerebroprotective; vulnerary;
KW cyostatic; immunosuppressive; virucide; antialcoholic; ss.

XX Spodoptera frugiperda.
OS
XX
FH Key Location/Qualifiers
FT CDS 229..1362
FT /*tag= a
FT /product= "Inhibitor of apoptosis protein"
FT /note= "CDS is referred as SEQ ID NO 2 in the
FT specification"

XX WO200159108-A2.
PN 16-AUG-2001.
XX
XX 07-FEB-2001; 2001WO-US004071.
PF 10-FEB-2000; 2000US-00502528.
XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 26, 2005, 16:56:56 ; Search time 86 Seconds
(without alignments)
1767.733 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAAATLVMLKN.....TDKPCNCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	1887	100.0	346	5	ABB78046
2	1311	69.5	377	4	AAE07881
3	767.5	40.7	263	5	ABH09488
4	721.5	38.2	438	4	AAE48189
5	719.5	38.1	438	4	ABB61858
6	719.5	38.1	438	4	ABB67347
7	719.5	38.1	438	4	AAE48188
8	719.5	38.1	438	4	AAE48190
9	719.5	38.1	438	8	ADO08093
10	713.5	37.8	438	4	AAE48192
11	713.5	37.8	438	4	AAE48191
12	711.5	37.7	438	4	AAE48196
13	709.5	37.6	438	4	AAE48197
14	708.5	37.5	438	4	AAE48193
15	708.5	37.5	438	4	AAE48194
16	532.5	28.2	434	4	AAE48195
17	526.5	27.9	604	2	AAW19747
18	526.5	27.9	604	2	AAW13546
19	526.5	27.9	604	2	AAW52703
20	526.5	27.9	604	2	AAW33997
21	526.5	27.9	604	6	ABU07431
22	526.5	27.9	604	6	ABB82739
23	526.5	27.9	604	7	ADB80948
24	526.5	27.9	604	7	AAE39811

25	526.5	27.9	604	8	ADG87135	Adg87135 Human CIA
26	526.5	27.9	604	8	ADH74643	Adh74643 Human CIA
27	526.5	27.9	604	8	ADS88171	Ads88171 Human pro
28	526.5	27.9	604	8	ADR89114	Adr89114 Human IAP
29	526.5	27.9	604	8	ADR67238	Adr67238 Human bla
30	526.5	27.9	604	8	ADU22899	Adu22899 Human apo
31	525.5	27.8	600	6	AAW69298	Aaw69298 Murine HI
32	525.5	27.8	600	6	ABP72155	Abp72155 Mouse inh
33	524.5	27.8	604	2	AAW19582	Aaw19582 Human apo
34	524.5	27.8	604	2	AAW69295	Aaw69295 Human HIA
35	524.5	27.8	604	5	ABG65664	Abg65664 Human inh
36	517.5	27.4	602	5	ABG65667	Abg65667 Mouse inh
37	516.5	27.4	602	2	AAW19585	Aaw19585 Mouse apo
38	507.5	26.9	618	2	AAW19583	Aaw19583 Human apo
39	507.5	26.9	618	2	AAW69296	Aaw69296 Human HIA
40	507.5	26.9	618	5	ABG65665	Abg65665 Human inh
41	501	26.6	497	7	ADI39803	Adi39803 Drosophil
42	500.5	26.5	496	2	AAW19745	Aaw19745 Mouse inh
43	500.5	26.5	618	2	AAW19746	Aaw19746 Human inh
44	500.5	26.5	618	2	AAW13545	Aaw13545 Human c-I
45	500.5	26.5	618	2	AAW33998	Aay33998 Human cel

ALIGNMENTS

RESULT 1	ABB78046	ABB78046 standard; protein; 346 AA.
ID	ABB78046	
AC	ABB78046;	
XX		
XX		
DT	22-OCT-2002 (first entry)	
XX		
DE	Amino acid sequence of inhibitor of apoptosis protein BmiAP.	
KW	Inhibitor of apoptosis protein; IAP; BmiAP; silkworm; apoptosis; insect;	
XX	Spodoptera frugiperda; insult-resistant plant; caspase.	
OS	Bombyx mori.	
FH	Key	Location/Qualifiers
FT	Domain	74..140
FT		/note= "BIR domain 1"
FT	Domain	182..249
FT		/note= "BIR domain 2"
FT	Domain	298..314
FT		/note= "RING domain"
XX		
PN	WO200253586-A2.	
XX		
PD	11-JUL-2002.	
XX		
PF	07-JAN-2002; 2002WO-US000314.	
XX		
PR	08-JAN-2001; 2001US-0260478P.	
XX		
PA	(BURN-) BURNHAM INST.	
XX		
PI	Maeda S, Huang Q, Reed JC, Deveraux QL;	
XX		
DR	WPI; 2002-590628/63.	
DR	N-PSDB; ABQ78228.	
XX		
PT	Novel recombinant polypeptide, inhibitor of apoptosis protein family	
PT	member BmiAP from silkworm Bombyx mori BmN cells, useful for inhibiting	
PT	apoptosis and identifying an agent that modulates activity of	
PT	polypeptide.	
XX		
PS	Claim 39; Page 31; 62pp; English.	
XX		
CC	The present score represents a polypeptide which is an inhibitor of	
CC	apoptosis protein (IAP) family member, and designated BmiAP. BmiAP is	

CC derived from silkworm Bombyx mori BmN cells. The BmiAP polypeptide
CC contains two baculoviral IAP repeat (BIR) domains, followed by a RING
CC domain. BmiAP polypeptides and polynucleotides are useful for inhibiting
CC apoptosis in insect cells, especially Spodoptera frugiperda or Bombyx
CC mori cells, and mammalian cells, and plant cells. They are also useful
CC for generating a biotic or abiotic insul-t-resistant plant. BmiAP is also
CC useful for inhibiting caspases
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1887; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 6.9e-174;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSCSSTSTLPSSSSADKTDNHD 60
Db 1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSCSSTSTLPSSSSADKTDNHD 60

QY 61 TFNFLPDMPMRREERLKTFDQWPVTLTPEQIARNGFYLLGRGDEVCCAFCKVEIMRW 120
Db 61 TFNFLPDMPMRREERLKTFDQWPVTLTPEQIARNGFYLLGRGDEVCCAFCKVEIMRW 120

QY 121 VEGDDPADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPRMPGVHARYS 180
Db 121 VEGDDPADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAAATQPRMPGVHARYS 180

QY 181 TEARLATFKDWPFRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKWESDDVPWEQHA 240
Db 181 TEARLATFKDWPFRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLKWESDDVPWEQHA 240

QY 241 RWFDRCAVYQVLVKGROYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDSKICK 300
Db 241 RWFDRCAVYQVLVKGROYIQVKSEATAISASEEQATNDSTKNVAQEGEKHLDSKICK 300

QY 301 ICYSEERNVCFVPCGHVVAACAKALSTDKCPMCRRTFTNAVRLYFS 346
Db 301 ICYSEERNVCFVPCGHVVAACAKALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 2
AAE07881 ID AAE07881 standard; protein; 377 AA.
XX
AC AAE07881;
DT 01-NOV-2001 (first entry)
XX
DE Fall armyworm inhibitor of apoptosis (IAP) protein.
XX
KW Fall armyworm; inhibitor of apoptosis; IAP; transgenic plant;
KW apoptosis inhibitor; therapy; acquired immune deficiency syndrome; AIDS;
KW neurodegenerative disease; Alzheimer's disease; aplastic anaemia;
KW Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
KW myelodysplastic syndrome; toxin-induced liver disease; ischaemic injury;
KW myocardial infarction; stroke; reperfusion injury; cancer; neurotic;
KW autoimmune disorder; lupus erythematosus; multiple sclerosis; vasotropic;
KW insecticide; viral infection; anti-HIV; human immunodeficiency virus;
KW neuroprotective; antianemic; cardiant; cerebroprotective; vulnerary;
KW cytoslatic; immunosuppressive; virucide; antialcoholic.
XX
OS Spodoptera frugiperda.
XX
PN WO200159108-A2.
XX
PD 16-AUG-2001.
XX
PF 07-FEB-2001; 2001WO-US004071.
XX
PR 10-FEB-2000; 2000US-00502528.
XX
PA (REGC) UNIV CALIFORNIA.
PA (MAED/) MAEDA H.
XX

PI Maeda S, Hammock BD, Huang Q, Maeda H;
XX
DR WPI; 2001-514667/56.
DR N-PSDB; AAD14419.
XX
PT Novel nucleic acid construct comprising cDNA encoding inhibitor of
PT apoptosis proteins, useful for controlling apoptosis in target cells and
PT for combating various disorders associated with apoptosis.
XX
PS Claim 6; Page 39; 43pp; English.
XX
CC The present sequence is fall armyworm inhibitor of apoptosis (IAP). The
CC IAP is useful for controlling apoptosis in target cells. It is also
CC useful for screening compounds that modulate apoptosis and for the
CC production of transgenic plants. The IAP can be used to delay, suppress
CC or inhibit an apoptosis response in plants. In animals, IAPs are used to
CC combat various disorders related to apoptosis, e.g., acquired
CC immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g.
CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis),
CC retinitis pigmentosa and other diseases of retina, myelodysplastic
CC syndrome (e.g. aplastic anaemia), toxin-induced liver diseases (e.g.
CC alcoholism), ischaemic injury (e.g. myocardial infarction, stroke and
CC reperfusion injury), cancers, autoimmune disorders (e.g. lupus
CC erythematosus and multiple sclerosis) and viral infections. The IAP is
CC also useful in vitro to monitor the expression of IAP cDNA, and to detect
CC the construction of recombinant baculoviruses that are useful as
CC insecticides
XX
SQ Sequence 377 AA;

Query Match 69.5%; Score 1311; DB 4; Length 377;
Best Local Similarity 68.5%; Pred. No. 5.5e-118;
Matches 248; Conservative 39; Mismatches 57; Indels 18; Gaps 7;

QY 1 MELTKVAKNGAAATLVMLKN-ARDAKMRPFIGPLML--SSCESSTSTLPSSS----- 51
Db 18 MDITKVASNGSSSTLTLFKSGSLFAKIRP-LAPLMLPTPSYDSNMGSPSLSPSTPCSSSS 76

QY 52 -SADKTDNHDTFENFLPDMPMRREERLKTFDQWPVTLTPEQIARNGFYLLGRGDEVCC 110
Db 77 FSIDKTDNHDTFEGFSADTVDMRKEDERMKTEKMPVSFLSGEQIARNGFYLLGRDEARC 136

QY 111 AFCKVEIMRWVEGDDPADHRRWAPQCPFVRKQMYANAGGEATAVGRDECGASAA--TQ 167
Db 137 AFCKVEIMRWVEGDDPAKDQRWAPQCPFVRK-LNGTAADTSSSGDECGARAAPSGTS 195

QY 168 PPRMPGVHARYSTEARLATFKDWPFRMRQKPEELAEAGFFYTGQDKTKCFYCDGGLK 227
Db 196 PPRMAGPVHPRYASEARLRFSKDWPRCMRQKPEELAEAGFFYTGQDKTKCFYCDGGLK 255

QY 228 DWESDDVPWEQHARWFDRCAYVQVLVKGROYIQVKSEATAISASEEQ---AATNDSTKN 284
Db 256 DWENHDVPWEQHARWFDRCAYVQVLVKGREYQKVISACEVSASEARDVAPARTAEPS 315

QY 285 VAQEGEKHLDSKICKICYSEERNVCFVPCGHVVAACAKALSTDKCPMCRRTFTNAVRLY 344
Db 316 PAEAPENSVDSSKICKICYAEBERNVCFVPCGHVVAACAKALAADKCPMCRRTFONAVRLY 375

QY 345 FS 346
Db 376 FS 377

RESULT 3
ABB09488 ID ABB09488 standard; protein; 263 AA.
XX
AC ABB09488;
XX
DT 01-JUL-2002 (first entry)
XX
DE AMEPV baculovirus-like inhibitor of apoptosis (AMV133).



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OM protein - protein search, using sw model

Run on: November 26, 2005, 17:25:31 ; Search time 109 Seconds
(without alignments)
2239.567 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAATVLMKN.....TDKCPMCRRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1887	100.0	346	Q968T8_BOMMO	Q968T8 bombyx mori
2	1866	98.9	346	Q8IS31_BOMMO	Q8IS31 bombyx mori
3	1327	70.3	379	Q9U492_TRINI	Q9U492 trichoplusi
4	1311	69.5	377	Q9N007_SPOFR	Q9N007 spodoptera
5	966	51.2	275	IAP_GVCP	P41436 cydia pomon
6	937	49.7	287	Q6E7G7_NPVAG	Q6E7G7 anticarsia
7	890.5	47.2	280	Q6VTV9_NPVCD	Q6VTV9 choristoneu
8	879	46.6	263	Q80SF4_NPVHC	Q80SF4 hyphantria
9	876	46.4	281	Q9YNI8_NPVCF	Q9YNI8 choristoneu
10	873	46.3	261	Q9QES9_NPVEP	Q9QES9 epiphyas po
11	873	46.3	276	Q89744_NPVBS	Q89744 buzura supp
12	862	45.7	268	IAP3_NPVOP	P41437 orgyia pseu
13	782	41.4	264	Q9EN27_AMEPV	Q9EN27 amasacta moo
14	747.5	39.6	255	Q7T5S1_GVCL	Q7T5S1 cryptophleb
15	728	38.6	313	Q9J827_9NUCL	Q9J827 spodoptera
16	719.5	38.1	438	IAP1_DROME	Q24306 drosophila
17	701	37.1	403	Q8WRD9_AEDTR	Q8WRD9 aedes trise
18	684	36.2	401	Q6Q507_AEDAE	Q6Q507 aedes aegyp
19	676.5	35.9	402	Q8T621_AEDAL	Q8T621 aedes albop
20	662	35.1	285	Q8UM16_9NUCL	Q8Jm16 mamestra co
21	653	34.6	276	Q71A73_9NUCL	Q71A73 mamestra co
22	653	34.6	276	Q8QL95_NPVMC	Q8QL95 mamestra co
23	635	33.7	283	Q80LK8_NPVAH	Q80LK8 adoxophyes
24	623.5	33.0	278	Q4KT41_9NUCL	Q4KT41 chrysodeixi
25	573	30.4	254	Q7T9S6_GVAO	Q7T9S6 adoxophyes
26	550	29.1	414	Q4T660_TETNG	Q4T660 tetraodon n
27	544.5	28.9	269	Q6QXJ6_GVAS	Q6QXJ6 agrotis seg
28	542	28.7	358	PIAP_PIG	Q62640 sus scrofa
29	538.5	28.5	304	Q5TW06_ANOGA	Q5TW06 anopheles g
30	532.5	28.2	268	Q9E232_9NUCL	Q9E232 heliocoverpa
31	530.5	28.1	401	Q8JHV9_XENLA	Q8JHV9 xenopus lae

32	530	28.1	186	2	Q7QJ55_ANOGA	Q7QJ55 anopheles g
33	529.5	28.1	268	2	Q77LW6_9NUCL	Q77LW6 heliocoverpa
34	529.5	28.1	268	2	Q9IF18_9NUCL	Q9IF18 heliocoverpa
35	528.5	28.0	602	2	Q9ESE9_RAT	Q9ESE9 rattus norv
36	526.5	27.9	602	2	Q5XIW4_RAT	Q5XIW4 rattus norv
37	526.5	27.9	604	1	BIRC3_HUMAN	Q13489 homo sapien
38	525.5	27.8	600	1	BIRC3_MOUSE	Q08863 mus musculu
39	520.5	27.6	604	2	Q6DDY3_XENLA	Q6DDY3 xenopus lae
40	516.5	27.4	616	2	Q804E2_ICTPU	Q804E2 ictalurus p
41	513.5	27.2	604	2	Q6GLD7_XENTR	Q6GLD7 xenopus tro
42	513	27.2	628	2	Q8UWD2_BRARE	Q8UWD2 brachydanio
43	513	27.2	647	2	Q7TOK2_BRARE	Q7TOK2 brachydanio
44	513	27.2	654	2	Q6ZM93_BRARE	Q6ZM93 brachydanio
45	511.5	27.1	639	2	Q4SFS0_TETNG	Q4SFS0 tetraodon n

ALIGNMENTS

RESULT 1									
Q968T8_BOMMO PRELIMINARY; PRT; 346 AA.									
ID	Q968T8;								
AC	Q968T8;								
DT	01-DEC-2001 (TREMBLrel. 19, Created)								
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)								
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)								
DE	Inhibitor of apoptosis protein.								
GN	Name=IAP;								
OS	Bombyx mori (Silk moth).								
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;								
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;								
OC	Bombycidae; Bombyx.								
OX	NCBI_TaxID=7091;								
RN	[1]								
RP	NUCLEOTIDE SEQUENCE.								
RX	MEDLINE=21240184; Pubmed=11341966; DOI=10.1016/S0167-4889(00)00105-1;								
RA	Huang Q., Deveraux Q.L., Maeda S., Stenmicke H.R., Hammock B.D.,								
RA	Reed J.C.;								
RT	"Cloning and characterization of an inhibitor of apoptosis protein								
RT	(IAP) from Bombyx mori.";								
RL	Biochim. Biophys. Acta 1499:191-198(2001).								
DR	EMBL; AF281073; AAK57560.1; -, mRNA.								
DR	HSSP; Q24306; 1Q4Q.								
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.								
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.								
DR	GO; GO:0008270; F:zinc ion binding; IEA.								
DR	GO; GO:0006916; P:anti-apoptosis; IEA.								
DR	GO; GO:0016567; P:protein ubiquitination; IEA.								
DR	InterPro; IPR001370; Prot_inh_I32_IAP.								
DR	InterPro; IPR001841; znf_ring.								
DR	Pfam; PF00653; BIR; 2.								
DR	SMART; SM00238; BIR; 2.								
DR	SMART; SM00184; RING; 1.								
DR	PROSITE; PS01282; BIR_REPEAT_1; 2.								
DR	PROSITE; PS50143; BIR_REPEAT_2; 2.								
DR	PROSITE; PS50089; ZF_RING_2; 1.								
SQ	SEQUENCE 346 AA; 38942 MW; 6CFC6C6468894C69 CRC64;								
Query Match 100.0%; Score 1887; DB 2; Length 346;									
Best Local Similarity 100.0%; Pred. No. 1.7e-144;									
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MELTKVAKNGAATVLMKNARDAKMRPFIGPLMLSSCESSSTSTLSPSSSADKTDNHD	60						
DB	1	MELTKVAKNGAATVLMKNARDAKMRPFIGPLMLSSCESSSTSTLSPSSSADKTDNHD	60						
QY	61	TNFFLPDMPDMRREERLKTFFDQWPVTLTPQLARNGFYLLGRGDEVCCAFCKVEIMRW	120						
DB	61	TNFFLPDMPDMRREERLKTFFDQWPVTLTPQLARNGFYLLGRGDEVCCAFCKVEIMRW	120						
QY	121	VEGDDPAADHRRWAPQCPEYRKQMYANAGGEATAVGRDECGASATQPPRMGPVYARYS	180						
DB	121	VEGDDPAADHRRWAPQCPEYRKQMYANAGGEATAVGRDECGASATQPPRMGPVYARYS	180						

QY 181 TEAARLATFKDWPFRMRQKPEELAEAGFFYTGQGDKTCTCYCDGGLKDWESDDVPWEQHA 240
DB 181 TEAARLATFKDWPFRMRQKPEELAEAGFFYTGQGDKTCTCYCDGGLKDWESDDVPWEQHA 240
QY 241 RWFDRCAVYQVLVKGRDYIQVKXSEATAISASEEQAAATNDSTKNVAQEGEKHLDDSKICK 300
DB 241 RWFDRCAVYQVLVKGRDYIQVKXSEATAISASEEQAAATNDSTKNVAQEGEKHLDDSKICK 300
QY 301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346
DB 301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 2
Q8IS31_BOMMO
ID Q8IS31_BOMMO PRELIMINARY; PRT; 346 AA.
AC Q8IS31;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Inhibitor of apoptosis protein.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang G., Wang L., Wu X.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY155274; AAN46650.1; -; mRNA.
DR HSSP; Q24306; 1Q4Q.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_I32_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 346 AA; 38849 MW; 5450EB75F56A8486 CRC64;

Query Match 98.9%; Score 1866; DB 2; Length 346;
Best Local Similarity 99.1%; Pred. No. 8.6e-143;
Matches 343; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSSTSTLSPSSSADKTDNHD 60
DB 1 MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSSTSTLSPSSSADKTDNHD 60
QY 61 TFNFLPDMPMRREERLKTFFDQWPVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRW 120
DB 61 TFNFLPDMPMRREERLKTFFDQWPVTLTPEQLARNGFYLLGRGDEVCCAFCKVEIMRW 120
QY 121 VEGDDPAADHRRWAPQCPFYRKQMYANAGGEATAVGRDECGASAAATQPRMPGVHARYS 180
DB 121 VEGDDPAADHRRWAPQCPFYRKQMYANAGGEAAAVGRDECGASAAATQPRMPGVHARYS 180
QY 181 TEAARLATFKDWPFRMRQKPEELAEAGFFYTGQGDKTCTCYCDGGLKDWESDDVPWEQHA 240
DB 181 TEAARLATFKDWPFRMRQKPEELAEAGFFYTGQGDKTCTCYCDGGLKDWESDDVPWEQHA 240
QY 241 RWFDRCAVYQVLVKGRDYIQVKXSEATAISASEEQAAATNDSTKNVAQEGEKHLDDSKICK 300
DB 241 RWFDRCAVYQVLVKGRDYIQVKXSEATAISASEEQAAATNDSTKNVAQEGEKHLDDSKICK 300
QY 301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

DB 301 ICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVRLYFS 346

RESULT 3
Q9U492_TRINI
ID Q9U492_TRINI PRELIMINARY; PRT; 379 AA.
AC Q9U492;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inhibitor of apoptosis protein.
GN Name=IAP1;
OS Trichoplusia ni (Cabbage looper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Plusiinae; Trichoplusia.
OX NCBI_TaxID=7111;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20062908; PubMed=10593985; DOI=10.1074/jbc.274.51.36769;
RA Seshagiri S., Vuclic D., Lee J., Dixit V.M.;
RT "Baculovirus-based genetic screen for antiapoptotic genes identifies a novel IAP.";
RL J. Biol. Chem. 274:36769-36773(1999).
DR EMBL; AF195528; AAF19819.1; -; mRNA.
DR HSSP; Q24306; 1Q4Q.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001370; Prot_inh_I32_IAP.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; 2.
DR PROSITE; PS50143; BIR_REPEAT_2; 2.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 379 AA; 41857 MW; 069381A012D9DE65 CRC64;

Query Match 70.3%; Score 1327; DB 2; Length 379;
Best Local Similarity 69.0%; Pred. No. 4.5e-99;
Matches 251; Conservative 39; Mismatches 54; Indels 20; Gaps 8;

QY 1 MELTKVAKNGAAATLVMLKNA-RDAKMRPFIGPLML--SSCESSSTSTLSPSS----- 51
DB 18 MDITKVASNGPASPULTLFKNAPRDAKIRPLV-PLVLPTQSYDSNAGSPASSPSTPSSSSS 76
QY 52 -SADKTDNHDTFNFLPDMPMRREERLKTFFDQWPVTLTPEQLARNGFYLLGRGDEVCC 110
DB 77 FSIDKTDNHDTFSLTADAVDMSREDERIKTFEKMVPSFLSGEQLARNGFYLLGRGDEVRC 136
QY 111 AFCKVEIMRWVEGDDPAADHRRWAPQCPFYRKQMYANAGGEATAVGRDECGASAA--TOP 168
DB 137 AFCKVEIMRWVEGDDPAKDQRWAPQCPFYRK--LGGGVNTDSGAAGRDECGARAAPTSSP 195
QY 169 PRMPGPVHARYSTEARLATFKDWPFRMRQKPEELAEAGFFYTGQGDKTCTCYCDGGLKD 228
DB 196 SRMPGPVHPRYASEARLRFSFKDWPFRMRQKPEELAEAGFFYTGQGDKTCTCYCDGGLKD 255
QY 229 WESDDVPWEQHARWFDRCAYVQVLVKGRDYIQVKXSEATAI--SASEE--QAATNDST 282
DB 256 WENDDVPEQHARWFDRCAYVQVLVKGREYQKVMTEACVIPAPAAPRDEAPARSAAPSV 315
QY 283 KNVAQEGEKHLDDSKICKICYSEERNVCFVPCGHVVACAKCALSTDKCPMCRRTFTNAVR 342
DB 316 VSAAPQESTLDDSKLCKICFAEERNVCFVPCGHVVACAKCALAADKCPMCRRTFQNAVR 375
QY 343 LYFS 346
DB 376 LYFS 379

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2005, 00:14:08 ; Search time 18362 Seconds
(without alignments)
11680.119 Million cell updates/sec

Title: US-10-041-859A-1
Perfect score: 3773
Sequence: 1 cattactaactcacttcac.....tgcggtctactctcgtga 3773

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3773	100.0	3773	6	AX664311	AX664311 Sequence
2	2716	72.0	2716	2	AF281073	AF281073 Bombyx mo
3	1033	27.4	1041	2	AY155274	AY155274 Bombyx mo
4	441.8	11.7	1739	2	AF186378	AF186378 Spodopter
5	441.8	11.7	1739	6	AR340174	AR340174 Sequence
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7	437.2	11.6	1134	6	AR340175	AR340175 Sequence
8	437.2	11.6	1134	6	AX213189	AX213189 Sequence
9	433.8	11.5	2614	2	AF195528	AF195528 Trichoplu
10	292.8	7.8	123500	13	US3466	US3466 Cydia pomon
11	270	7.2	1247	13	AY525121	AY525121 Anticarsi
12	254	6.7	1032	13	CFU82510	U82510 Choristoneu
13	254	6.7	129593	13	AF512031	AF512031 Choriston
14	226.6	6.0	1386	13	NPHIAP	L22564 Orygia pseu
15	226.6	6.0	131995	13	OPU75930	U75930 Orygia pseu
16	226.2	6.0	3248	13	AF045936	AF045936 Buzura su
17	218.6	5.8	131160	13	AY327402	AY327402 Choriston
18	208.2	5.5	1241	13	AB088850	AB088850 Hyphantri

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C	20	200.6	5.3	118584	13	AY043265	AY043265 Epiphyas
C	21	161	4.3	110907	13	AY229987	AY229987 Cryptophl
C	22	142.4	3.8	50000	6	AX392733	AX392733 Sequence
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C	24	130.4	3.5	794	6	AX392714	AX392714 Sequence
C	25	130	3.4	113220	13	AP006270	AP006270 Adoxophye
C	26	120.6	3.2	135611	13	AF169823	AF169823 Spodopter
C	27	117	3.1	134394	13	DQ017380	DQ017380 Trichoplu
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C	29	113.6	3.0	266	2	AY751528	AY751528 Spodopter
C	30	112.4	3.0	133877	14	AC120883	AC120883 Homo sapi
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C	36	109.2	2.9	258658	2	AE014832	AE014832 Plasmodiu
C	37	109	2.9	135121	8	AC069525	AC069525 Homo sapi
C	38	108.2	2.9	348174	2	CR382399	CR382399 Plasmodiu
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C	41	107	2.8	86826	2	PFMAL3P5	AL034556 Plasmodiu
C	42	106.4	2.8	4601	2	DMU11584	U11584 Drosophila
C	43	106.4	2.8	19517	2	DMU37541	U37541 Drosophila
C	44	106.2	2.8	1662	2	AF447592	AF447592 Ochlerota
C	45	105.8	2.8	254050	2	PFA929358	AL929358 Plasmodiu

ALIGNMENTS

RESULT 1
AX664311
LOCUS AX664311 3773 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1 from Patent WO02053586.
ACCESSION AX664311
VERSION AX664311.1 GI:29164241
KEYWORDS
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
REFERENCE 1
AUTHORS Huang,Q., Reed,J.C., Devereaux,Q.L. and Maeda,S.D.
TITLE Inhibitor of apoptosis proteins and nucleic acids and methods for making and using them
JOURNAL Patent: WO 02053586-A 1 11-JUL-2002;
The Burnham Institute (US)
FEATURES
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ORIGIN

Query Match 100.0%; Score 3773; DB 6; Length 3773;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	TTTAGTGTCTACTCGGTCTGTCTGCGTGCCTGACGTTTGGAACTTCATATTTTG	120
Db	61	TTTAGTGTCTACTCGGTCTGTCTGCGTGCCTGACGTTTGGAACTTCATATTTTG	120
QY	121	TTCTTGCAAGACGAGTGTCACTGATTAAACAAAAACATAAGATAGACGTTTATGCGTT	180
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 26, 2005, 17:43:17 ; Search time 6043 Seconds
(without alignments)
3254.647 Million cell updates/sec

Title: US-10-041-859A-2
Perfect score: 1887
Sequence: 1 MELTKVAKNGAATLVMLKN.....TDKCPMCRKRTFTNAVRLYFS 346

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1887	100.0	2716	2	AF281073	Bombyx mo
2	1887	100.0	3773	6	AX664311	Sequence
3	1866	98.9	1041	2	AY155274	Bombyx mo

4	1327	70.3	2614	2	AF195528	AF195528 Trichopl
5	1311	69.5	1134	6	AR340175	AR340175 Sequence
6	1311	69.5	1134	6	AX213189	AX213189 Sequence
7	1311	69.5	1739	2	AF186378	AF186378 Spodopt
8	1311	69.5	1739	6	AR340174	AR340174 Sequence
9	1311	69.5	1739	6	AX213188	AX213188 Sequence
10	966	51.2	123500	13	U53466	U53466 Cydia pomon
11	937	49.7	1247	13	AY525121	AY525121 Anticarsi
12	890.5	47.2	131160	13	AY327402	AY327402 Choriston
13	884	46.8	129593	13	AF512031	AF512031 Choriston
14	879	46.6	1241	13	AB088850	AB088850 Hyphantri
15	876	46.4	1032	13	CFU82510	U82510 Choristoneu
16	873	46.3	1787	13	AF180757	AF180757 Epiphyas
17	873	46.3	3248	13	AF045936	AF045936 Buzura su
18	873	46.3	118584	13	AY043265	AY043265 Epiphyas
19	862	45.7	1386	13	NP81AP	L22564 Orgyia pseu
20	862	45.7	131995	13	OPU75930	U75930 Orgyia pseu
21	787	41.7	50000	6	AX392733	AX392733 Sequence
22	787	41.7	232392	13	AF250284	AF250284 Amsacta m
23	748	39.6	794	6	AX392714	AX392714 Sequence
24	747.5	39.6	110907	13	AY229987	AY229987 Cryptophl
25	728	38.6	135611	13	AF169823	AF169823 Spodopt
26	725.5	38.4	1317	6	AR432086	AR432086 Sequence
27	723.5	38.3	1317	6	AR432085	AR432085 Sequence
28	723.5	38.3	1317	6	AR432087	AR432087 Sequence
29	723.5	38.3	2017	2	DR0D1AP1X	L49440 Drosophila
30	719.5	38.1	1858	6	CQ601074	CQ601074 Sequence
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34	719.5	38.1	85633	14	AC014423	AC014423 Drosophil
35	719.5	38.1	169209	2	AC093499	AC093499 Drosophil
36	719.5	38.1	176056	2	AC010066	AC010066 Drosophil
37	719.5	38.1	283815	2	AE003528	AE003528 Drosophil
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40	715.5	37.9	1317	6	AR432093	AR432093 Sequence
41	713.5	37.8	1317	6	AR432094	AR432094 Sequence
42	712.5	37.8	1317	6	AR432090	AR432090 Sequence
43	712.5	37.8	1317	6	AR432091	AR432091 Sequence
44	712	37.7	1662	2	AF447592	AF447592 Ochlerota
45	707	37.5	1484	2	AY119524	AY119524 Drosophil

ALIGNMENTS

RESULT 1	AF281073	2716 bp	mRNA	linear	INV 30-MAY-2001
LOCUS	Bombyx mori	inhibitor of apoptosis protein (IAP) mRNA, complete			
DEFINITION	cds.				
ACCESSION	AF281073				
VERSION	AF281073.1	GI:14248545			
KEYWORDS					
SOURCE					
ORGANISM	Bombyx mori (domestic silkworm)				
REFERENCE					
AUTHORS	Huang,Q., Deveraux,Q.L., Maeda,S., Stennicke,H.R., Hammock,B.D. and Reed,J.C.				
TITLE	Cloning and characterization of an inhibitor of apoptosis protein				
JOURNAL	(IAP) from Bombyx mori				
PUBMED	Biochim. Biophys. Acta 1499 (3), 191-198 (2001)				
REFERENCES	11341966				
AUTHORS	2 (bases 1 to 2716)				
TITLE	Huang,Q., Deveraux,Q.L., Maeda,S., Salvesen,G.S., Stennicke,H.R., Hammock,B.D. and Reed,J.C.				
JOURNAL	Direct Submission				
FEATURES	Submitted (21-JUN-2000) Entomology, University of California at Davis, One Shields Avenue, Davis, CA 95616, USA				
	location/Qualifiers				

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ORIGIN

Alignment Scores: Pred. No.: 1.37e-126 Length: 2716 Score: 1887.00 Matches: 346 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 2 Gaps: 0

US-10-041-859A-2 (1-346) x AF281073 (1-2716)

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DB 266 GCGCGGATGCAGAAATGCGACCTTTCATGTGCTCCGCTCATGTTATCCCTGCTGAGTCT 325
QY 41 SerThrThrSerThrIeuProSerProSerSerSerAlaAspIysThrAspAsnHisAsp 60
DB 326 TCAACGACATCCACACTCCCGTCACCTTCGTCGTCAGCTGATAAACGATATACACGAC 385
QY 61 ThrPheAsnPheIeuProAspMetProAspMetArgGluGluIuArgIeuIysThr 80
DB 386 ACATTCACTTCCTTCGATATGCCCGACATGCGTCGTGAAGAGAACGTGTGAATAACA 445
QY 81 PheAspGlnTrpProValThrPheLeuThrProGluGlnIleuAlaArgAsnGlyPheTyr 100
DB 446 TTTGATCAGTGGCCCGTTACGTTTGTGACGCCGGAACAATTGGCCCCGCAACGATTTCTAC 505
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DB 506 TACCTCGGTGCGGCGAGAGTGTGCTGTGCTTCTGTAAAGGTAGAAATATAGAGGTGG 565
QY 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140
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DB 746 ACCGAGCGCGCGGCTGCCCACTTCAAGACTGGCGGAGACGTATGCGCCAAAAACCC 805
QY 201 GluGluLeuAlaGluIaGlyPhePheTyrThrGlyGlnGlyAspIysThrIysCysPhe 220

DB 806 GAGAACTGGCAGAGCCGGATTCTTCTATACAGGCCAAGGTGACAAAAAGAAATGCTTC 865
QY 221 TyrCysAspGlyGlyLeuIysAspTrpGluSerAspAspValProTrpGluGlnHisAla 240
DB 866 TATTGCGACGAGGGCTAAAGATTGGGAAAGCATGACGTTCCGTGGGAACAGCAGCC 925
QY 241 ArgTrpPheAspArgCysAlaTyrValGlnIleuValIysGlyArgAspTyrIleGlnIys 260
DB 926 AGATGTTCCGACCGCTGCCGCTACGTCAATTGCTGAAGAGACGTGACTACATTCAAGAG 985
QY 261 ValIysSerGluAlaThrAlaIleSerAlaSerGluGluGluGlnAlaAlaThrAsnAsp 280
DB 986 GTGAAGTCGAGGCCCACTGCGATATCTGCTAGCGAAGAAAGAACAGGCCGCCCAATGAT 1045
QY 281 SerThrIysAsnValAlaGlnGlyGlyIuIysHisIleuAspAspSerIysIleCysIys 300
DB 1046 TCGACTAAGAACGTGCGCCCAAGAGGCGGAGAAACATTGGATGACTCTAAAAATATGTAAA 1105
QY 301 IleCysTrpSerGluGluArgAsnValCysPheValProCysGlyHisValAlaIaCys 320
DB 1106 ATATGTTATTCGAGAGAGCGTAACTGTGCTTCGTGCGGCGCACGTTGGTGGCTGC 1165
QY 321 AlaIysCysAlaIleuSerThrAspIysCysPrometCysArgArgThrPheThrAsnAla 340
DB 1166 GCCAAGTCGCGCTGTCGACGCAAGTGCCTGCTGTCGACGACGTTCAAGATGCG 1225
QY 341 ValArgLeuTyrPheSer 346
DB 1226 GTGCGGCTTACTTCTCG 1243

RESULT 2
AX664311 3773 bp DNA linear PAT 22-MAR-2003
LOCUS
DEFINITION Sequence 1 from Patent WO02053586.
ACCESSION AX664311
VERSION AX664311.1 GI:29164241
KEYWORDS
SOURCE
ORGANISM Bombyx mori (domestic silkworm)
Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.

REFERENCE 1
Huang, Q., Reed, J.C., Deveraux, Q.L. and Maeda, S.D.
Inhibitor of apoptosis proteins and nucleic acids and methods for
making and using them
Patent: WO 02053586-A 1 11-JUL-2002;
The Burnham Institute (US)
Location/Qualifiers

FEATURES
source 1. .3773 /organism="Bombyx mori" /mol_type="unassigned DNA" /db_xref="taxon:7091" 2733. .3773 /note="unnamed protein product" /codon_start=1 /protein_id="CAD80028.1" /db_xref="GI:29164242" /translation="MELTKVAKNGAAATLVMLKNARDAKMRPFIGPLMLSSCESSTTS TLPSSSADKTDNHDTFNFLPDMRREERLKTFDQWPVTFILTPQIARNGFYLL GRGDEVCCAFCKVEIMRWEGDDPADHRWAPQCFVRKOMYANAGGEATAVGRDEC GASAAIQPRMGPVHARYSTEARLATFKDWRMRQKPEELAEAGFFYTGQDKTK CFYCDGLKDWESDVPWEQHARWFDRCAYVQLVKGRDYIQVKSSEATAIISASEEQ AATNDSTKNVAQEGEKHLDSKICKICYSEERNVCFVPCGHVAVCAKCALSTDKCPMCR RTFTNAVRLYFS"

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ORIGIN
Alignment Scores: Pred. No.: 2.01e-126 Length: 3773 Score: 1887.00 Matches: 346 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0

DB:	6	Gaps:	0
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Db	206	ATGGAAGTTGACGAAAGTTGCTAAATAATGAGCTGCCGCCACGTTGGTATGTTAAAAAT	265
QY	21	AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer	40
Db	266	GCGCGGGATGCAAAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGTGAGTCT	325
QY	41	SerThrThrSerThrLeuProSerProSerSerSerSerAlaAspLysThrAspAsnHisAsp	60
Db	326	TCAACGACATCCACACTCCCGCTCACCTTCGTGTCAGCTGATAAAAACGGATATATCAGAC	385
QY	61	ThrPheAsnPheLeuProAspMetProAspMetArgGluGluGluLysThr	80
Db	386	ACATTCAACTTCCTTCGTATATGCCGACATGCGTGTGAAGAGAACGTTGAAAAACA	445
QY	81	PheAspGlnTrpProValThrPheLeuThrProGluGlnLeuAlaArgAsnGlyPheTyr	100
Db	446	TTTGATCAGTGCGCCGTTACGTTTGTGACGCCGGAACAATTGGCCCGCAACGGAATCTAC	505
QY	101	TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysLysValGluIleMetArgTrp	120
Db	506	TACCTCGGTGCGCGCGACGAAGTGTGCTGTCTTCTGTAAAGTAGAATATAGAGTGG	565
QY	121	ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal	140
Db	566	GTCGAAGCGCAGCATCTTGCCCGCATCATCGAGATGGCGCCCGCAGTGTCCCTTTGTA	625
QY	141	ArgLysGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys	160
Db	626	CGAAAACAATGTATGCTCAACGCTGGGGAGAGAGCGACCGCTGTGCTAGAGACGAATGT	685
QY	161	GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer	180
Db	686	GGGGCCAGTGCGGCCACGACCTCCCGCATGCCCGCCCGTGCACGCGCGTACTCC	745
QY	181	ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro	200
Db	746	ACCGAGGCGCGCGCTCGCACCTTCAAGACTGCGCGAGACGTATGCCCAAAAAACC	805
QY	201	GluGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPhe	220
Db	806	GAGGAAGCTGGCAGAGGCCGGAATCTTCTATACAGGCCCAAGGTGACAAAAAGAAATGCTTC	865
QY	221	TyrCysAspGlyGlyLeuLysAspTrpGluSerAspAspValProTrpGluGlnHisAla	240
Db	866	TATTGCGACGGAGGGCTTAAAGATTGGGAAAAGCATGACGTTCCGTGGAAACAGCAGCC	925
QY	241	ArgTrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLys	260
Db	926	AGATGTTTCGACCGCTGCGCTGCAATTGCTGAAGGACGTGACTACATTCAAG	985
QY	261	ValLysSerGluAlaThrAlaIleSerAlaSerGluGluGlnAlaAlaThrAsnAsp	280
Db	986	GTAAGTCGAGGCCACTGCGATATCTGTAGCGAAGAGAACAGGCCCAACCAATGAT	1045
QY	281	SerThrLysAsnValAlaGlnGluGlyGluLysHisLeuAspAspSerLysIleCysLys	300
Db	1046	TCGACTAAGAAGCTGCCCAAGAGGGCGAAGAACATTTGGATGACTCTAAATATGTAAA	1105
QY	301	IleCysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValValAlaCys	320
Db	1106	ATATGTTATTCCGAGGAGCGTAACTGTGCTTCGTGCCGTGCGCCACGTTGTTGGCTGC	1165
QY	321	AlaLysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAla	340
Db	1166	GCCAAGTGCCTGTGTGACGGCAAGTGCCCGATGTGTGCGAGGACGTTACGGAATCGG	1225
QY	341	ValArgLeuTyrPheSer	346

Db	1226	GTGCGGCTCTACTTCTCG	1243
RESULT 3			
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LOCUS	AY155274		
DEFINITION	Bombyx mori inhibitor of apoptosis protein mRNA, complete cds.		
ACCESSION	AY155274		
VERSION	AY155274.1	GI:24286570	
KEYWORDS			
SOURCE	Bombyx mori (domestic silkworm)		
ORGANISM	Bombyx mori		
REFERENCE	1 (bases 1 to 1041)		
AUTHORS	Yang,G., Wang,L. and Wu,X.		
TITLE	A novel isoform of inhibitor of apoptosis from lepidoptera Bombyx mori (BmIAPv)		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1041)		
AUTHORS	Yang,G., Wang,L. and Wu,X.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-SEP-2002) Functional Gene and Biotechnology, Shanghai Biochemistry and Cell Biology Chinese Academy of Sciences, 320 Yue-Yang road, Shanghai 200031, People's Republic of China		
FEATURES	location/Qualifiers		
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CDS			
ORIGIN			
Alignment Scores:			
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Query Match:	98.89%	Indels:	0
DB:	2	Gaps:	0
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Db	1	ATGGAAGTTGACGAAAGTTGCTAAATAATGAGCTGCCGCCACGTTGGTATGTTAAAAAAT	60
QY	21	AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeuSerSerCysGluSer	40
Db	61	GCGCGGATGCAAAAATGCGACCTTTCATTGGTCCGCTCATGTTATCCTCGTGCAGTCT	120
QY	41	SerThrThrSerThrLeuProSerProSerSerSerSerAlaAspLysThrAspAsnHisAsp	60
Db	121	TCAACGACATCCACACTCCCGTCACCTTCGTGTCAGCTGATAAAAACGATATCAGAC	180
QY	61	ThrPheAsnPheLeuProAspMetProAspMetArgGluGluGluLysThr	80

Db 181 ACATTCAACTTCTCTTCTGTATATGCCCGACATGCGTCTGTAAGAGGAACGCTCTGAAAAACA 240

QY 81 PheAspGlnTrpProValThrPheLeuThrProGlnLeuAlaArgAsnGlyPheTyr 100

Db 241 TTGTATCAGTGGCCCGTTACGTTTGTAGCGCCGGAACAATTGGCCCGCAACGGAATTCTAC 300

QY 101 TyrLeuGlyArgGlyAspGluValCysCysAlaPheCysValGluIleMetArgTrp 120

Db 301 TACCTCGGTGCGCGCGACGAAGTGTGTGTCTTCTGTAAAGTAGAAATTATGAGGTGG 360

QY 121 ValGluGlyAspAspProAlaAlaAspHisArgArgTrpAlaProGlnCysProPheVal 140

Db 361 GTCGAAGCGCAGATCCTGCCCGCATCATCGAGATGGCGCCCGCAGTGTCTTGTGA 420

QY 141 ArgLySGlnMetTyrAlaAsnAlaGlyGlyGluAlaThrAlaValGlyArgAspGluCys 160

Db 421 CGAAAAACAATGTATGCCAACGCTGGGGGAGAGCGCGCTGTCCGTAAGACGAATGT 480

QY 161 GlyAlaSerAlaAlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSer 180

Db 481 GGGGCCAGTGGCCCGCACGACCTTCCCGCATGCCCGCCCGCTGCACCGCGCTACTCC 540

QY 181 ThrGluAlaAlaArgLeuAlaThrPheLyAspTrpProArgArgMetArgGlnLyPro 200

Db 541 ACCGAGCGCGCGCTGCCACCTTCAAGGACTGCGCGAGATGTATGCGCAAAACC 600

QY 201 GlnGluLeuAlaGluAlaGlyPhePheTyrThrGlyGlnGlyAspLyThrCysCysPhe 220

Db 601 GAGGAAGTGGCAGAGCGCGGATTTCTTCTATACAGCCAAAGTGACAAAACGAATGCTTC 660

QY 221 TyrCysAspGlyGlyLeuLyAspTrpGlySerAspAspValProTrpGlnGlnHisAla 240

Db 661 TATTGCGACGAGGCGCTAAAGATTGGGAAGCGATGACGTTCCGTGGGAACGACGCC 720

QY 241 ArgTrpPheAspArgCysAlaTyrValGlnLeuValLySGlyArgAspTyrIleGlnLyS 260

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QY 261 ValLySerGlnAlaThrAlaIleSerAlaSerGlnGlnGlnAlaAlaThrAsnAsp 280

Db 781 GTGAAGTCGAGGCGCACTGCGATATCTGTAAGCAAGAACAGGCCCGCCCAATGAT 840

QY 281 SerThrLyAsnValAlaGlnGlnGlyGlyLyHisLeuAspAspSerLyIleCysLyS 300

Db 841 TCGACTAAGAACGTGCTCAAGAGGCGGAGAAACAATTGGATGACTTAATAATGTAA 900

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QY 321 AlaLySCysAlaLeuSerThrAspLyCysProMetCysArgArgThrPheThrAsnAla 340

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QY 341 ValArgLeuTyrPheSer 346

Db 1021 GTGCGGCTCTACTTCTCG 1038

RESULT 4

AF195528 2614 bp mRNA linear INV 26-DEC-1999

LOCUS Trichoplusia ni inhibitor of apoptosis protein (IAP1) mRNA, complete cds.

ACCESSION AF195528

VERSION AF195528.1 GI:6635436

KEYWORDS Trichoplusia ni (cabbage looper)

SOURCE Trichoplusia ni

ORGANISM Trichoplusia ni

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyosia; Noctuoidea; Noctuidae; Plusiinae; Trichoplusia.

REFERENCE 1 (bases 1 to 2614)

AUTHORS Seshagiri, S., Vucic, D., Lee, J. and Dixit, V.M.

TITLE Baculovirus-based genetic screen for antiapoptotic genes identifies a novel IAP

JOURNAL J. Biol. Chem. 274 (51), 36769-36773 (1999)

PUBMED 10593985

REFERENCE 2 (bases 1 to 2614)

AUTHORS Seshagiri, S., Vucic, D., Lee, J. and Dixit, V.M.

TITLE Direct Submission

JOURNAL Submitted (15-OCT-1999) Molecular Oncology, Genentech Inc., 1 DNA Way, San Francisco, CA 94080, USA

FEATURES

source

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123. .1262

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ORIGIN

Alignment Scores:

Pred. No.: 3,06e-86 Length: 2614

Score: 1327.00 Matches: 251

Percent Similarity: 79.67% Conservative: 39

Best Local Similarity: 68.96% Mismatches: 54

Query Match: 70.32% Indels: 20

DB: 2 Gaps: 8

US-10-041-859A-2 (1-346) x AF195528 (1-2614)

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Db 174 ATGATATTAACCAAGTGGCATCCATGGCCCCCTCACCATTAACACTTTTCAAGAAG 233

QY 21 Ala--ArgAspAlaLySMetArgProPheIleGlyProLeuMetLeu-----SerSer 37

Db 234 GCTCCGCGCGAGCTTAAGATTGCACTCTAGTG--CCGCTAGTGTGGCCGACGACAGAGC 290

QY 38 CysGluSerSerThrThrSerThrLeuProSerProSerSer----- 51

Db 291 TACGACTCAACGCCCGGCTCTCCGGCTTCCTCACCCTCACACCTCATCGTCTTCTCA 350

QY 52 ---SerAlaAspLySThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAsp 70

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Db 471 GGGGAGCACTGCGCCGAAACGGAATTCTATTACCTTGGCCGCGAGATGAGGTCCGATGC 530

QY 111 AlaPheCysLySValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130

Db 531 GCTTCTGCAAGTCGAATCATGAGATGGGTGAGGCTGACGACCAACGAAGATCAC 590

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QY	169	ProArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThr	188		
Db	708	TCTCGCATGCTTGGCCCTGTTCACCCGCTTATGCTCTGAAGCCCGCGCTTGCAGAT	767		
QY	189	PhelyAspTrpProArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGlyPhe	208		
Db	768	TTTAAAGACTGGCCAGATGCGGACAGAACGCCGAGAGCTGGCTGAGGCTGATTC	827		
QY	209	PheTyrThrGlyGlnGlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLysAsp	228		
Db	828	TTTTCACATGCTCAGGCGCGATTAAGACGAATGCTTTATTTGATGCTGGCCCTGAAGAT	887		
QY	229	TrpGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAlaTyr	248		
Db	888	TGGGAAAAAGACGACGTCGCTGGGAGCAACACGCGCGTGTTCAGCCGCTGCGTTAC	947		
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QY	283	LysAsnValAlaGlnGluGlyLysHisLeuAspAspSerLysIleCysLysIleCys	302		
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QY	303	TyrSerGluGluValArgAsnValCysPheValProCysGlyHisValValAlaCysAlaLys	322		
Db	1128	TTGCTGAGGAGCGCAATGTGTCTTCTGTCGCTGTGCCACGTGTGGCGTGTCTAAG	1187		
QY	323	CysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAlaValArg	342		
Db	1188	TGCGCGCTGCGACGCCAGACAGTCCGATGTGCCGAGGACGTTTCAGAAATGCAATGCGG	1247		
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LOCUS	AR340175	Sequence 2 from patent US 6570069.			
ACCESSION	AR340175				
VERSION	AR340175.1	GI:33731574			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1134)				
AUTHORS	Hammock,B.D., Huang,Q. and Maeda,S.				
TITLE	Nucleic acids encoding plant inhibitors of apoptosis and transgenic				
JOURNAL	cells and plants expressing them				
FEATURES	Patent: US 6570069-A 2 27-MAY-2003;				
source	Location/Qualifiers				
ORIGIN	1..1134				
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Alignment Scores:					
Pred. No.:	1.65e-85	Length:	1134		
Score:	1311.00	Matches:	248		
Percent Similarity:	79.28%	Conservative:	39		
Best Local Similarity:	68.51%	Mismatches:	57		

Query Match:	69.48%	Indels:	18
DB:	6	Gaps:	7
US-10-041-859a-2 (1-346) x AR340175 (1-1134)			
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Db	52	ATGATATTATCCAAAGTGGCATCCAAATGGCTCTCCTCAACATTTAACGCTATTCAAGAC	111
QY	21	---AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeu-----SerSer	37
Db	112	GGATCGCTTGAGGCTAAATTCGACCT--CTGGCCCACTAATGCTGCCGACGCCAAGT	168
QY	38	CysGluSerSerThrThrSerThrLeuProSerProSerSer-----	51
Db	169	TACGACTCCAACCGCGCTCTCCATCTTGTCTCCATCCACGCCCTTGCTTCATCTTCT	228
QY	52	---SerAlaAspLysThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAsp	70
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Db	289	ATGAGAAAAGAGATGAACGTATGAACAATTGAAAATGCCCCGTAAGTTTCTATCC	348
QY	91	ProGluGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys	110
Db	349	GGAGAGCAACTGTCTGAAATGGAATTTACTACTTCGCGCTGAGAGATGAAGCCCGTTGC	408
QY	111	AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis	130
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QY	131	ArgArgTrpAlaProGlnCysProPheValArgLysGlnMetTyrAlaAsnAlaGlyGly	150
Db	469	CAGCGTTGGCGCCACAGTCCCATTTGTGCGCAA---TTGAACGTTACTGACGACGA	525
QY	151	GIuAlaThraValaIGlyArgAspGluCysGlyAlaSerAlaala-----ThrGln	167
Db	526	GACACGGGTAGTTCGGGCCAGAGACGAGTGTGTCGCCGCGCTCCCTCCGGTACTCT	585
QY	168	ProProArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAla	187
Db	586	CCGCCCGTATGCGCGGTCCGTGCCACCACGATATGCATCTGAAGCCGACGACTACGC	645
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Db	646	AGTTTAAAGACTGGCCACGATGCATGCGACAAAACCTGAAGAACTCGCCGAGCTGCG	705
QY	208	PhePheTyrThrGlyGlnGlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLys	227
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QY	248	TyrValGlnLeuValLysGlyArgAspTyrIleGlnLysValLysSerGluAlaThrAla	267
Db	826	TACGTCAATTGTGAAGGTCGAGAAATACGTCAAAAAGTGATTCTGAAGCTTGTGAG	885
QY	268	IleSerAlaSerGluGluGln-----AlaAlaThrAsnAspSerThrLysAsn	284
Db	886	GTAATCCGCTCAGAACGCGAAGCTGATGACACCCGACGAGCTGCCGAGCAAGCCCG	945
QY	285	ValAlaGlnGluGlyGlyLysHisLeuAspAspSerLysIleCysLysIleCysTyrSer	304
Db	946	CCAGCAGAGCGCCAGAAAACCTCAGTCGATGACTCAAGTTGTGTAATAATCTGTATGCT	1005
QY	305	GluGluValArgAsnValCysPheValProCysGlyHisValAlaCysAlaLysCysAla	324
Db	1006	GAAAGCGTAACGTGTCTTCTGTCGCGCGGACGTTGTGGCTTGCGCCAGTGCGCG	1065

QY 325 LeuSerThrAspIysCySPrometCySArgArgThrPheThrAsnAlaValArgLeuTyr 344
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Db 1066 CTGGCGGCCGACAGTGCCTCATGTGCGCAGACGTTTCAAATGACAGTGGGTATAT 1125

QY 345 pheSer 346
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Db 1126 TTCTCG 1131

RESULT 6
AX213189 1134 bp DNA linear PAT 06-SEP-2001
LOCUS Sequence 2 from Patent WO0159108.
DEFINITION AX213189
ACCESSION AX213189
VERSION AX213189.1 GI:15524134
KEYWORDS
SOURCE
ORGANISM
Spodoptera frugiperda (fall armyworm)
Spodoptera frugiperda
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyritinae; Spodoptera.

REFERENCE
AUTHORS
TITLE
JOURNAL
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
Patent: WO 0159108-A 2 16-AUG-2001;
Inhibitors of apoptosis
Maeda,S.D., Huang,Q. and Maeda,H.E.

FEATURES
source
1. .1134
Location/Qualifiers
/organism="Spodoptera frugiperda"
/mol_type="unassigned DNA"
/db_xref="taxon:7108"
/note="SfiAP nucleotide sequence, open reading frame (ORF)
only"
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/note="unnamed protein product; fall armyworm inhibitor of
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POCFVRKLNGTAAADTGSSGDECGARAPSGTSPRMAGPVHPRYASBARLRSFK
DWPRCMRQKPELEAAGFFYTGQDKTKFCYCDGLKDWENHDVPWQHARWFDRCAY
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AERNVCFVPCGHVVAACAKALADKCPMCRRTFQNAVRLYFS"

ORIGIN
Alignment Scores:
Pred. No.: 1.65e-85 Length: 1134
Score: 1311.00 Matches: 248
Percent Similarity: 79.28% Conservative: 39
Best Local Similarity: 68.51% Mismatches: 57
Query Match: 69.48% Indels: 18
DB: 6 Gaps: 7
US-10-041-859A-2 (1-346) x AX213189 (1-1134)

QY 1 MetGluLeuThrIysValAlaIalysAsnGlyAlaAlaIaThrLeuValMetLeuIysAsn 20
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QY 21 ---AlaArgAspAlaIysMetArgProPheIleGlyProLeuMetLeu-----SerSer 37
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QY 38 CysGluSerSerThrIysSerThrLeuProSerProSerSer----- 51
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Db 169 TACGACTCCAAACGCGGCTCTCCATCTTTGCTCCATCCACGCCCTTGCTTCACTTCT 228

QY 52 ---SerAlaAspIysThrAspAsnHisAspThrPheAsnPheLeuProAspMetProAsp 70
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Db 229 TTCTCCATTGATAAACCGACGACACGACACCTTCGGCTTCAGTGGGACACAGTTGAT 288

QY 71 MetArgArgGluGluGluArgLeuIysThrPheAspGlnTrpProValThrPheLeuThr 90
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Db 289 ATGAGAAAGAGATGAACGATATGAATAATGCGCCGTAAGTTTCTATCC 348

QY 91 ProGluGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCysCys 110
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QY 111 AlaphCySlySValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
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Db 409 GCTTCTGTAAAGTGAAGATTATGAGGTGGTGAGGGCGATGACCTGCGAAGACCAT 468

QY 131 ArgArgTrpAlaProGlnCysProPheValArgIysGlnMetTyrAlaAsnAlaGlyGly 150
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QY 151 GluAlaThrAlaValGlyArgAspGluCysGlyAlaSerAlaAla-----ThrGln 167
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Db 526 GACACGGGTAGTTCGGGCCACAGACGAGTGTGTCGCCGCGCTCCCTCCGTTACCTCT 585

QY 168 ProProArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAla 187
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Db 586 CCGCCGCGTATGGCCCGGTCCCGTGACACCCACGATATGCATCTGAAGCCGACGACTACGC 645

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QY 228 AspTrpGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAla 247
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Db 766 GATTGGAGAACCATGACGTACCCCTGGGAACAACAGCAAGGTGTTGACCGTGGCC 825

QY 248 TyrValGlnLeuValIysGlyArgAspTyrIleGlnIysValIysSerGluAlaThrAla 267
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QY 268 IleSerAlaSerGluGluGln-----AlaAlaThrAsnAspSerThrIysAsn 284
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QY 285 ValAlaGlnGluGlyGluIysHisLeuAspAspSerIysIleCysIysIleCysTyrSer 304
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QY 305 GluGluArgAsnValCysPheValProCysGlyHisValAlaCysAlaIysCysAla 324
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Db 1006 GAAGAGCGTAACGTGTGCTTGCGTCCGCGGCCACGTCGTGCTGCGCCAAGTGGCGG 1065

QY 325 LeuSerThrAspIysCySPrometCySArgArgThrPheThrAsnAlaValArgLeuTyr 344
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QY 345 pheSer 346
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Db 1126 TTCTCG 1131

RESULT 7
AF186378 1739 bp mRNA linear INV 23-FEB-2000
LOCUS Spodoptera frugiperda inhibitor of apoptosis protein (IAP) mRNA,
DEFINITION complete cds.
ACCESSION AF186378
VERSION AF186378.1 GI:7021324
KEYWORDS
SOURCE
ORGANISM
Spodoptera frugiperda (fall armyworm)
Spodoptera frugiperda
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyritinae; Spodoptera.


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REFERENCE      1 (bases 1 to 1739)
AUTHORS        Huang,Q., Deveraux,Q.L., Maeda,S., Salvesen,G.S., Stennicke,H.R.,
                Hammock,B.D. and Reed,J.C.
TITLE          Evolutionary conservation of apoptosis mechanisms: lepidopteran and
                baculoviral inhibitor of apoptosis proteins are inhibitors of
                mammalian caspase-9
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1427-1432 (2000)
PUBMED         10677478
REFERENCE      2 (bases 1 to 1739)
AUTHORS        Huang,Q., Deveraux,Q.L., Maeda,S., Salvesen,G.S., Stennicke,H.R.,
                Hammock,B.D. and Reed,J.C.
TITLE          Direct Submission
JOURNAL        Submitted (15-SEP-1999) The Burnham Institute, 10901 North Torrey
                Pines Road, La Jolla, CA 92037, USA
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ORIGIN
Alignment Scores:
Pred. No.:      2.71e-85      Length:      1739
Score:          1311.00      Matches:      248
Percent Similarity: 79.28%      Conservative: 39
Best Local Similarity: 68.51%      Mismatches: 57
Query Match:    69.48%      Indels:      18
DB:             2           Gaps:       7
US-10-041-859A-2 (1-346) x AFI186378 (1-1739)
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Db      280 ATGATATTACCAAGTGCATCCATGGCTCCTCCTCAACATTAAAGCTATTCAAGAGC 339
QY      21 ---AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeu-----SerSer 37
        :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      340 GGATCGCTTAGGCTAAATTCGACCT--CTCGCGCACATAATGCTGCCGACGCCAAGT 396
QY      38 CysGluSerSerThrThrSerThrLeuProSerProSerSer-----51
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Db      397 TAGCACTCCAACGCCGCTCTCCATCTTGTCTCCATCCACGCCCTTGCTTCACTTCT 456
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Db      457 TTCTTCATTGATAAACCGACCAACACGACACACCTTCGGCTTCAGTGGGACACAGTTGAT 516
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QY      111 AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
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Db      754 GACACGGGTAGTTCGGGCGACGAGCAGAGTGTTGGTCCCGCGCTCCTCCGGTACCTCT 813
QY      168 ProProArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAla 187
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QY      188 ThrPheLysAspTrpProArgArgMetArgGlnLysProGluGluAlaGluAlaGly 207
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QY      208 PhePheTyrThrGlyGlnGlyAspLysThrLysCysBheTyrCysAspGlyGlyLeuLys 227
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QY      228 AspTrpGluSerAspAspValProTrpGluGlnHisAlaArgTrpPheAspArgCysAla 247
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Db      994 GATTGGAGAACCATGACGTACCCCTGGGAACAACGCAAGGTGTTTGACCGTTGCGCC 1053
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Db      1054 TACGTGCAATTGGTGAAGGGTCCGAGAATACGTTCAAAGGTGATTTCTGAAGCTTGTGAG 1113
QY      268 IleSerAlaSerGluGluGluGln-----AlaAlaThrAsnAspSerThrLysAsn 284
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QY      285 ValAlaGlnGluGlyLysHisLeuAspAspSerLysIleCysLysIleCysTyrSer 304
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Db      1174 CCAGCAGAGCGCCGCAAGAACTCAGTCGATGACTCAAAAGTTGTAAATCTGTATGCT 1233
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Db      1234 GAAGAGCGTAACGTGTCTTCGTGCGCGTGCAGCGTGTGCTTGCGCAAGTGCAGCG 1293
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RESULT 8
LOCUS      AR340174 1739 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6570069.
ACCESSION  AR340174
VERSION     AR340174.1 GI:33731573
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1739)
AUTHORS    Hammock,B.D., Huang,Q. and Maeda,S.
TITLE      Nucleic acids encoding plant inhibitors of apoptosis and transgenic
                cells and plants expressing them
JOURNAL    Patent: US 6570069-A 1 27-MAY-2003;
                Regents of the University of California; Oakland, CA
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ORIGIN
Alignment Scores:

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Pred. No.: 2.71e-85 Length: 1739
Score: 1311.00 Matches: 248
Percent Similarity: 79.28% Conservative: 39
Best Local Similarity: 68.51% Mismatches: 57
Query Match: 69.48% Indels: 18
DB: 6 Gaps: 7

US-10-041-859A-2 (1-346) x AR340174 (1-1739)

QY 1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaThrLeuValMetLeuLysAsn 20
DB ATGGATATTACCAAGTGGCATCCAAATGGCTCTCTCAACATTAAACGCTATTCAAGAGC 339
QY 21 --AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeu-----SerSer 37
DB GGATCGCTTGAGGCTAAAAATTGCACCT--CTCGCGCCACTAAATGCTGCCGACGCCAAGT 396
QY 38 CysGluSerSerThrThrSerThrLeuProSerProSerSer----- 51
DB TACGACTCCAAAGCCGGCTCTCCATCTTTGTCTCCATCCACGCCCTTGCTCTCATCTTCT 456
QY 52 ---SerAlaAspLysThrAspAsnHisAspThrPheAsnPhleuProAspMetProAsp 70
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QY 111 AlaPheCysLysValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHis 130
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QY 131 ArgArgTrpAlaProGlnCysProPheValArgLysGlnMetTyrAlaAsnAlaGlyGly 150
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QY 168 ProProArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAla 187
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QY 345 PheSer 346
DB TTCTCG 1359

RESULT 9
AX213188 1739 bp DNA linear PAT 06-SEP-2001
LOCUS AX213188
DEFINITION Sequence 1 from Patent WO0159108.
ACCESSION AX213188
VERSION AX213188.1 GI:15524132
KEYWORDS
SOURCE
ORGANISM
Spodoptera frugiperda (fall armyworm)
Spodoptera frugiperda
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyritinae; Spodoptera.

REFERENCE
AUTHORS Maeda,S.D., Huang,Q. and Maeda,H.E.
TITLE Inhibitors of apoptosis
JOURNAL Patent: WO 0159108-A 1 16-AUG-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)

FEATURES
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ORIGIN

Alignment Scores:

Pred. No.: 2.71e-85 Length: 1739
Score: 1311.00 Matches: 248
Percent Similarity: 79.28% Conservative: 39
Best Local Similarity: 68.51% Mismatches: 57
Query Match: 69.48% Indels: 18
DB: 6 Gaps: 7

US-10-041-859A-2 (1-346) x AX213188 (1-1739)

QY 1 MetGluLeuThrLysValAlaLysAsnGlyAlaAlaThrLeuValMetLeuLysAsn 20
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QY 21 --AlaArgAspAlaLysMetArgProPheIleGlyProLeuMetLeu-----SerSer 37
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ORGANISM	
Cydia pomonella granulovirus	
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
AUTHORS	1 (bases 1 to 123500)
TITLE	Crook,N.E., Clem,R.J. and Miller,L.K.
	An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif
JOURNAL	J. Virol. 67 (4), 2168-2174 (1993)
PUBMED	8445726
REFERENCE	2 (bases 1 to 123500)
AUTHORS	Theilmann,D.A., Chantler,J.K., Stewart,S., Flipsen,H.T., Viak,J.M. and Crook,N.E.
TITLE	Characterization of a highly conserved baculovirus structural protein that is specific for occlusion-derived virions
JOURNAL	Virology 218 (1), 148-158 (1996)
PUBMED	8615018
REFERENCE	3 (bases 1 to 123500)
AUTHORS	Kang,W., Crook,N.E., Winstanley,D. and O'Reilly,D.R.
TITLE	Complete sequence and transposon mutagenesis of the BamHI J fragment of Cydia pomonella granulosis virus
JOURNAL	Virus Genes 14 (2), 131-136 (1997)
PUBMED	9237352
REFERENCE	4 (bases 1 to 123500)
AUTHORS	Kang,W., Tristem,M., Maeda,S., Crook,N.E. and O'Reilly,D.R.
TITLE	Identification and characterization of the Cydia pomonella granulovirus cathepsin and chitinase genes
JOURNAL	J. Gen. Virol. 79 (Pt 9), 2283-2292 (1998)
PUBMED	9747739
REFERENCE	5 (bases 1 to 123500)
AUTHORS	Luque,T., Finch,R., Crook,N., O'Reilly,D.R. and Winstanley,D.
TITLE	The complete sequence of the Cydia pomonella granulovirus genome
JOURNAL	J. Gen. Virol. 82 (Pt 10), 2531-2547 (2001)
PUBMED	11562546
REFERENCE	6 (bases 1 to 123500)
AUTHORS	Crook,N.E.
TITLE	Direct Submission
JOURNAL	Submitted (11-JUN-1993) Entomological Sciences, Horticulture Research International, Wellesbourne, Warwickshire CV35 9EF, UK
REFERENCE	7 (bases 1 to 123500)
AUTHORS	Crook,N.E.
TITLE	Direct Submission
JOURNAL	Submitted (08-JAN-1996) Entomological Sciences, Horticulture Research International, Wellesbourne, Warwickshire CV35 9EF, UK
REFERENCE	8 (bases 1 to 123500)
AUTHORS	Kang,W., Crook,N.E., Winstanley,D. and O'Reilly,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (03-APR-1996) Imperial College of Science, Technology and Medicine, Imperial College Road, SAF Building, 5th floor, London SW7 2AZ, UK
REFERENCE	9 (bases 1 to 123500)
AUTHORS	Crook,N.E., James,J.D., Smith,I.R.L. and Winstanley,D.
TITLE	Direct Submission
JOURNAL	Submitted (15-NOV-1996) Entomological Sciences, Horticulture Research International, Wellesbourne, Warwickshire CV35 9EF, UK
REFERENCE	10 (bases 1 to 123500)
AUTHORS	Kang,W.
TITLE	Direct Submission
JOURNAL	Submitted (02-FEB-1998) Lab. of Mol. Entomol. and Baculovirol., RIKEN, 2-1 Hiroxawa, Wako, Saitama 351-0198, Japan
REFERENCE	11 (bases 1 to 123500)
AUTHORS	Luque,T., Finch,R., Crook,N., O'Reilly,D.R. and Winstanley,D.
TITLE	Direct Submission
JOURNAL	Submitted (03-APR-2001) Imperial College of Science, Technology and Medicine, Imperial College Road, SAF Building, 5th floor, London SW7 2AZ, UK
REMARK	Sequence update by submitter
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QY	181	ThrGluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysPro	200
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DEFINITION	Anticarsia gemmatalis nucleopolyhedrovirus IAP-3 gene, complete cds.		
ACCESSION	AY525121		
VERSION	AY525121.1	GI:46401441	
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ORGANISM	Nucleopolyhedrovirus.		
REFERENCE	1 (bases 1 to 1247)		
AUTHORS	Carpes,M.P., Castro,M.E., Soares,E.F., Villela,A.G., Pinedo,F.J. and Ribeiro,B.M.		
TITLE	Characterization of the inhibitor of apoptosis gene (iap-3) gene of Anticarsia gemmatalis multicapsid nucleopolyhedrovirus (AgMPV) Unpublished		
JOURNAL	2 (bases 1 to 1247)		
REFERENCE	Carpes,M.P., Castro,M.E., Soares,E.F., Villela,A.G., Pinedo,F.J. and Ribeiro,B.M.		
AUTHORS	Submitted (13-JAN-2004) Cell Biology, University of Brasilia, Campus Universitario Darcy Ribeiro UnB, Brasilia, DF 70910-900, Brazil		
TITLE	Direct Submission		
JOURNAL	Submitted (13-JAN-2004) Cell Biology, University of Brasilia, Campus Universitario Darcy Ribeiro UnB, Brasilia, DF 70910-900, Brazil		
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US-10-041-859A-2 (1-346) x AY327402 (1-131160)

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Db	23641	GGCCTCAAGACTGGGAAGCACCGACGAGCCGTGGGAAGAACACGACGACGCTTGTGAT	23582
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Db	23581	CGCTGCACATACGTGCGCTCGTAAAGGCTACGACTACGTCAACGCGTGTGCAAA	23522
QY	265	AlaThrAlaIleSerAlaSerGlu-----GluGluGlnAlaAlaThrAsnAspSerThr	282
Db	23521	GCGTGCCTCATTTAAAGAAAGAAACGTTGAGCAGCTCCGCAAGCTTAAACGTGCCAGAA	23462
QY	283	LysAsnVal---AlaGlnGluGlyGluLysHisIleLeuAspAspSerLysIleCysLysIle	301
Db	23461	GAAACAACGAGTGTGTTGAGCAGACCGCTTGACGTTGCGCAAGAAATGTGCAAGATT	23402
QY	302	CysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValAlaCysAla	321
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QY	322	LysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAlaVal	341
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RESULT 13
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LOCUS
DEFINITION Choristoneura fumiferana MNPV polynedrin, complete genome.

ACCESSION AF512031 AF177329 S46001 S78506 S81690 U10441 U18677 U26676 U26734
VERSION U53854 U57401 U59008 U70432 U72240 X65395
KEYWORDS AF512031.3 GI:57903534
SOURCE .
ORGANISM Choristoneura fumiferana MNPV
Choristoneura fumiferana MNPV
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
REFERENCE 1 (bases 1 to 129593)
AUTHORS lee,H.Y., Arif,B., Dobos,P. and Krell,P.
TITLE Identification of bent DNA and ARS fragments in the genome of
Choristoneura fumiferana nuclear polyhedrosis virus
JOURNAL Virus Res. 24 (3), 249-264 (1992)
PUBMED 1413988
REFERENCE 2 (bases 1 to 129593)
AUTHORS Xie,W.D., Arif,B., Dobos,P. and Krell,P.J.
TITLE Identification and analysis of a putative origin of DNA replication
in the Choristoneura fumiferana multinucleocapsid nuclear
polyhedrosis virus genome
JOURNAL Virology 209 (2), 409-419 (1995)
PUBMED 7778276
REFERENCE 3 (bases 1 to 129593)
AUTHORS Liu,J.J. and Carstens,E.B.
TITLE Identification, localization, transcription, and sequence analysis
of the Choristoneura fumiferana nuclear polyhedrosis virus DNA
polymerase gene
JOURNAL Virology 209 (2), 538-549 (1995)
PUBMED 7778286
REFERENCE 4 (bases 1 to 129593)
AUTHORS Barrecl,J.W., Krell,P.J. and Arif,B.M.
TITLE Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
viruses isolated from Choristoneura fumiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
PUBMED 7595348
REFERENCE 5 (bases 1 to 129593)
AUTHORS Qiu,W., Liu,J.J. and Carstens,E.B.
TITLE Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene
expression in insect cells
JOURNAL Virology 217 (2), 564-572 (1996)
PUBMED 8610448
REFERENCE 6 (bases 1 to 129593)
AUTHORS Liu,J.J. and Carstens,E.B.
TITLE Identification, molecular cloning, and transcription analysis of
the Choristoneura fumiferana nuclear polyhedrosis virus
spindle-like protein gene
JOURNAL Virology 223 (2), 396-400 (1996)
PUBMED 8806578
REFERENCE 7 (bases 1 to 129593)
AUTHORS Lapointe,R., Back,D.W., Ding,Q. and Carstens,E.B.
TITLE Identification and molecular characterization of the Choristoneura
fumiferana multicapsid nucleopolyhedrovirus genomic region encoding
the regulatory genes pkip, p47, lef-12, and gta
JOURNAL Virology 271 (1), 109-121 (2000)
PUBMED 10814576
REFERENCE 8 (bases 1 to 129593)
AUTHORS Carstens,E.B., Liu,J.J. and Dominy,C.
TITLE Identification and molecular characterization of the baculovirus
CfMNPV early genes: le-1, le-2 and pe38
JOURNAL Virus Res. 83 (1-2), 13-30 (2002)
PUBMED 11864738
REFERENCE 9 (bases 1 to 129593)
AUTHORS de Jong,J.G., Lauzon,H.A., Dominy,C., Poloumienko,A.,
Carstens,E.B., Arif,B.M. and Krell,P.J.
TITLE Analysis of the Choristoneura fumiferana nucleopolyhedrovirus
genome
J. Gen. Virol. 86 (Pt 4), 929-943 (2005)
PUBMED 15784887
REFERENCE 10 (bases 1 to 129593)
AUTHORS de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2002) Department of Microbiology, University of

REFERENCE 11 (bases 1 to 129593)
AUTHORS de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2004) Department of Microbiology, University of
Guelph, Chemistry and Microbiology Building, Guelph, ON N1G 2W1,
Canada
REMARK Sequence update by submitter
REFERENCE 12 (bases 1 to 129593)
AUTHORS de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2005) Department of Microbiology, University of
Guelph, Chemistry and Microbiology Building, Guelph, ON N1G 2W1,
Canada
REMARK Sequence update by submitter
COMMENT On Jan 19, 2005 this sequence version replaced gi:47157118.
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YFICK"

CDS

Alignment Scores:

Pred. No.:	2.41e-52	Length:	129593
Score:	884.00	Matches:	176
Percent Similarity:	62.25%	Conservative:	45
Best Local Similarity:	49.58%	Mismatches:	102
Query Match:	46.85%	Indels:	32
DB:	13	Gaps:	6

US-10-041-859A-2 (1-346) x AF512031 (1-129593)

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QY 35 leuSerSerCysGluSerSerThrThrSerThrLeuProSerProSerSerSerAlaAsp 54

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QY 55 LysThrAspAsnHisAspThrPheAsnPhelLeuProAspMetProAspMetArgGlu 74

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QY 115 ValGluIleMetArgTrpValGluGlyAspAspProAlaAlaAspHisArgArgTrpAla 134

Db 25309 GTGGAAGATTATGCGCTGGGAGCGCGGCGGACGACCGGCTCGCATCATCAAAATGGCGG 25250

QY 135 ProGluCysProPheValArgLySglMetTyraIaAsnAlaGlyGlyGluAlaThrAla 154

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QY 155 ValGlyArgAspGluCysGlyAlaSerAla-----AlaThrGluProPro 169

Db 25207 GCGCGGCAAGACGTCAGAGTTTGACCGCGCGGCAAGAACGTGAAGCAACAATCAACTG 25148

QY 170 ArgMetProGlyProValHisAlaArgTySerThrGluAlaAlaArgLeuAlaThrPhe 189

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Db 24847 GACACAACCAAAACAAGTT-----GTTAAGCATACGTTTAC----- 24809

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QY 310 CysPheValProCysGlyHisValValAlaCysAlaLysCysAlaLeuSerThrAspLys 329

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RESULT 14

AB088850 1241 bp DNA linear VRL 24-JUN-2004

LOCUS Hyphantria cunea nucleopolyhedrovirus gene for HcIAP-3, complete cds.

DEFINITION

ACCESSION AB088850

VERSION AB088850.1 GI:27923007

KEYWORDS

SOURCE

ORGANISM

Hyphantria cunea nucleopolyhedrovirus

Hyphantria cunea nucleopolyhedrovirus

Viruses; dsDNA viruses, no RNA stage; Baculoviridae;

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCES
AUTHORS
TITLE
JOURNAL

Nucleopolyhedrovirus.
Ikeda, M., Yanagimoto, K. and Kobayashi, M.
Identification and functional analysis of Hyphantiria cunea
nucleopolyhedrovirus iap genes
Virology 321 (2), 359-371 (2004)
15051395
2 (bases 1 to 1241)
Ikeda, M. and Kobayashi, M.
Direct Submission
Submitted (26-JUL-2002) Motoko Ikeda, Nagoya University, Graduate
School of Bioagricultural Sciences, Chikusa-ku, Nagoya, Aichi
464-8601, Japan (E-mail:mochikoeagr.nagoya-u.ac.jp,
Tel:81-52-789-4038, Fax:81-52-789-4038)
Location/Qualifiers

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ORIGIN
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Pred. No.: 2.54e-54 Length: 1241
Score: 879.00 Matches: 154
Percent Similarity: 70.65% Conservative: 41
Best Local Similarity: 55.80% Mismatches: 61
Query Match: 46.58% Indels: 20
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US-10-041-859A-2 (1-346) x AB088850 (1-1241)
QY 70 AspmetAArgGluGluGluArgLeuLysThrPheAspGlnTrpProValThrPheLeu 89
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QY 90 ThrProGluGlnLeuAlaArgAsnGlyPheTyrTyrLeuGlyArgGlyAspGluValCys 109
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QY 110 CysAlaPheCysLysValGluIleMetArgTyrValGluGlyAspAspProAlaAlaAsp 129
Db 316 TCGCGCTTTTGCAAAGTGAATAATATGCGTTGGCTTGAGGGGTGACGACCCGCGTTGAC 375
QY 130 HisArgArgTTrpAlaProGlnCysPProPheValArgLysGlnMetTyrAlaAsnAlaGly 149
Db 376 CATAAAGATTAGCGCCACAGTGTCCGTTCAAT----- 408
QY 150 GlyGluAlaThrAlaValGlyArgAspGluCysGlyAlaSerAlaAlaThrGlnProPro 169
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QY 170 ArgMetProGlyProValHisAlaArgTyrSerThrGluAlaAlaArgLeuAlaThrPhe 189
Db 454 -----CCCGTGCATCCCAATAACGCAACGGAAGTGCACGTTTGCACACTTTT 501
QY 190 LysAspTrpProArgArgMetArgGlnLysProGluGluLeuAlaGluAlaGlyPhePhe 209
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QY 210 TyrThrGlyGlnGlyAspLysThrLysCysPheTyrCysAspGlyGlyLeuLysAspTrp 229
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QY 230 GluSerAspAspValProTrpGluGlnHisAlaArgTTrpPheAspArgCysAlaTyrVal 249
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QY 270 AlaSerGluGluGlnAlaAlaThrAsnAspSerThrLysAsnValAlaGlnGluGly 289
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RESULT 15
CFU82510 1032 bp DNA linear VRL 05-JAN-1999
LOCUS
DEFINITION
Choristoneura fumiferana nucleopolyhedrovirus apoptosis inhibitor
(IAP) gene, complete cds.
VERSION
U82510
U82510.1 GI:4099075

SOURCE
ORGANISM
Choristoneura fumiferana MNPV
Choristoneura fumiferana MNPV
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 1032)
Lauzon, H., Arif, B.M., Ladd, T. and Palli, R.
cfMNPV IAP gene
Unpublished

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1032)
Lauzon, H., Arif, B.M., Ladd, T. and Palli, R.
Direct Submission
Submitted (17-DEC-1996) NRCan, Forestry Canada, 1219 Queen St. E,
Box 490, Sault Ste. Marie, Ont P6A 5M7, Canada

FEATURES
source
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Location/Qualifiers

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ORIGIN
Alignment Scores:

Pred. No.: 3.37e-54 Length: 1032
 Score: 876.00 Matches: 159
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 Query Match: 46.42% Indels: 18
 DB: 13 Gaps: 4

US-10-041-859A-2 (1-346) x CFU82510 (1-1032)

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QY 87 ThrphLeuThrProgluInleuAlaargasnilypHeTyrTyrLeuGlyArgGlyAsp 106
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QY 147 AsnAlaGlyGlyGluAlaThrAlaValGlyArgaspGluCysGlyAlaSerAla----- 164
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 299 -----AGCGCGCGCACTGTGTCTGCGCGCGCAAGACGTGCAGGTTTGCACGCGCGCAA 352
QY 165 -----AlaThrGlnProProArgMetProGlyProValHisAlaArgTyrSerThr 181
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 353 GAACGTGAAGCAACAATCAACTGCCCTCTCCGCCACCGCGCACCCCAATATGCGATA 412
QY 182 GluAlaAlaArgLeuAlaThrPheLysAspTrpProArgArgMetArgGlnLysProGlu 201
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 413 GAACTGCGCGTTTGCGCACATTACAGAGTGCGCACGCGTTTGAAGCAACGCGCGAA 472
QY 202 GluLeuAlaGlyAlaGlyPhePheTyrThrGlyGlnGlyAspLysThrLysCysPheTyr 221
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 473 AAACCTGCAGAGCTGGCTCTTTTACACCGCGCGGTAGCGACAAGTCAATGTTTAC 532
QY 222 CysAspGlyGlyLeuLysAspTrpGluSerAspValProTrpGluGlnHisAlaArg 241
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 533 TCGGACGCGCGTTTGCAACTGGGAGCAAGATGACGACCGGTGGCAACACGCGCTT 592
QY 242 TrpPheAspArgCysAlaTyrValGlnLeuValLysGlyArgAspTyrIleGlnLysVal 261
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 593 TGGTTCGGCGCTGCGCATACGTACTTGTCAAGGCGCGGATTATGTACAAAGGTC 652
QY 262 LysSerGluAlaThrAlaIleSerAlaSerGluGluGlnAlaAlaThrAsnAspSer 281
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 653 GTGACCGAATCGTGCATTCGCGACACACCAAAACAAAGTT----- 697
QY 282 ThrLysAsnValAlaGlnGluGlyLysHisLeuAspAspSerLysIleCysLysIle 301
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 698 GTTAAGCATACGGTTAC-----GAACCAATCTGCCCGATGAAGAAGCTTGCAGATT 751
QY 302 CysTyrSerGluGluArgAsnValCysPheValProCysGlyHisValAlaCysAla 321
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 752 TGCTATTACGATGAATAATCGTGTGCTTCGTGCCGCGCATGTGTAGCGTGGCGC 811
QY 322 LysCysAlaLeuSerThrAspLysCysProMetCysArgArgThrPheThrAsnAlaVal 341
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 812 AAGTGGCGGTCAATTCAGCAATTCGCCCATATGCCGTGCACCGTGAAACTGCCGTT 871
QY 342 ArgLeuTyr 344
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 872 CGCATGTAC 880
    
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